```
                                GenCore version 5.1.7
                        Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:         February 1, 2006, 13:19:06 ; Search time 53.4986 Seconds
                                                         (without alignments)
                                                         2961.978 Million cell updates/sec

Title:          US-09-888-264-1
Perfect score:  2181
Sequence:       1 ccgaggggccattgatgggcg...........ctccattgaggactcaataaa 1123

Scoring table:  BLOSUM62
                Xgapop  10.0 ; Xgapext  0.5
                Ygapop  10.0 ; Ygapext  0.5
                Fgapop   6.0 ; Fgapext  7.0
                Delop    6.0 ; Delext   7.0

Searched:       2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters:         4332886

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US09888264/runat_01022006_131838_14779/app.query.fasta_1
-DB=UniProt -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US0988264 @CGN_1.1_580 @runat_01022006_131838_14779 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -LONGLOG
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7 -FGAPOP=6 -FGAPEXT=7

Database :  UniProt
            1:  uniprot_sprot:*
            2:  uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1600	73.4	314	2	Q6IBH0_HUMAN	Q6ibh0 homo sapien
2	1600	73.4	314	2	Q5RFJ5_PONPY	Q5rfj5 pongo pygma
3	1595	73.1	313	2	M2OM_HUMAN	homo sapien
4	1558	71.4	314	2	Q5SX53_MOUSE	mus musculu
5	1553	71.2	313	2	M2OM_MOUSE	mus musculu
6	1549	71.0	314	1	Q5E9W4_BOVIN	bos taurus
7	1544	70.8	313	1	M2OM_BOVIN	bos taurus
8	1535	70.4	313	1	M2OM_RAT	rattus norv
9	1418	65.0	305	2	P97700_RAT	rattus norv
10	1407	64.5	305	2	Q566L1_XENTR	xenopus tro
11	1382	63.4	308	2	Q6INH3_XENLA	xenopus lae
12	1363	62.5	313	2	Q6IQ89_BRARE	brachydanio
13	1258	57.7	252	2	Q4TA26_TETNG	tetraodon n
14	1064	48.8	307	2	Q9CTC7_MOUSE	mus musculu
15	1052	48.2	306	2	Q61QH3_CAEBR	caenorhabdi
16	957	43.9	193	2	P90992_CAEEL	caenorhabdi
17	915.5	42.0	317	2	Q9VAJ9_DROME	drosophila
18	891.5	40.9	292	2	Q5TN06_ANOGA	anopheles g
19	839.5	38.5	311	2	Q9V293_DROME	drosophila
20	838.5	38.4	311	2	Q8SXB4_DROME	drosophila
21	782	35.9	301	2	Q9V294_DROME	drosophila
22	716	32.8	318	2	Q54PY7_DICDI	dictyosteli
23	608	27.9	309	2	Q53PA7_ORYSA	oryza sativ
24	606	27.8	307	2	Q66PW8_SACOF	saccharum o
25	602.5	27.6	302	2	Q42422_PANMI	panicum mil
26	598	27.4	302	2	Q40918_PANMI	panicum mil
27	597	27.4	299	2	Q6T871_9ROSI	citrus juno
28	596	27.3	313	2	Q59IV3_MESCR	mesembryant
29	596	27.3	321	2	Q6YX13_ORYSA	oryza sativ
30	591	27.1	298	2	Q8SF02_TOBAC	nicotiana t
31	590	27.0	300	2	Q66PX3_SACOF	saccharum o
32	589	27.0	325	2	Q66PX3_SACOF	saccharum o
33	587	26.9	297	2	Q8SF04_TOBAC	nicotiana t
34	587	26.9	306	2	Q60EY9_ORYSA	oryza sativ
35	585	26.8	295	2	Q8SF03_TOBAC	nicotiana t
36	585	26.8	295	2	Q9C5M0_ARATH	arabidopsis
37	583	26.7	297	2	Q8SF01_TOBAC	nicotiana t
38	583	26.7	313	2	Q9FSF4_TOBAC	nicotiana t
39	581	26.6	313	2	Q43649_SOLTU	solanum tub
40	579	26.6	313	2	Q9SJY5_ARATH	arabidopsis
41	574	26.3	313	2	Q66PX4_SACOF	saccharum o
42	571.5	26.2	319	2	Q81DF6_ARATH	arabidopsis
43	565.5	25.9	319	2	Q94K32_ARATH	arabidopsis
44	561.5	25.7	319	2	Q7RMU4_PLAYO	plasmodium
45	556	25.5	285	2	Q4XPT4_PLACH	plasmodium
				2	Q4YBX9_PLABE	plasmodium
				2	Q7QBN6_ANOGA	anopheles g

ALIGNMENTS

```
RESULT 1
Q6IBH0_HUMAN
ID   Q6IBH0_HUMAN PRELIMINARY;        PRT;   314 AA.
AC   Q6IBH0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   SLC25A11 protein.
GN   Name=SLC25A11;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CR456834; CAG33115.1; -; mRNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR   GO; GO:0005488; F:binding; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
KW   Transmembrane; Transport.
SQ   SEQUENCE   314 AA;  34061 MW;  9D61F8170B9FF5AA CRC64;

Alignment Scores:
Pred. No.:                 1.68e-106       Length:           314
Score:                     1600.00         Matches:          313
Percent Similarity:        100.0%          Conservative:       1
Best Local Similarity:     99.7%           Mismatches:         0
Query Match:               73.4%           Indels:             0
                                           Gaps:               0

DB:  US-09-888-264-1 (1-1123) x Q6IBH0_HUMAN (1-314)

Qy  21 ATGGCGGCGGACGACGCGAGTGCCGGGGCCGGGGCCGGCGGGGATGGACGGGAAGCCCGTACCTCCCCT 80
        |||||||||||||||||||||||||||||||||||||||||||||||||||::|||||||||||||
Db   1 MetAlaAlaThrAlaSerAlaGlyAlaGlyAlaGlyGlyAspGlyLysProArgThrSerPro 20
```

```
OC   Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Heart;
RG   The German cDNA Consortium;
RA   Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA   Han M., Wiemann S.;
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CR857161; CAH89462.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR   GO; GO:0005488; F:binding; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR002113; Aden_trnslctor.
DR   InterPro; IPR001993; Mitch_carrier.
DR   Pfam; PF00153; Mito_carr; 3.
DR   PRINTS; PR00927; ADPTRNSLCASE.
DR   PROSITE; PS50920; SOLCAR; 3.
KW   Hypothetical protein; Transport.
SQ   SEQUENCE   314 AA;   34047 MW;  9BCC4C637F8130FA CRC64;
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Alignment Scores:

Pred. No.:	
Score:	1600.00
Percent Similarity:	100.0%
Best Local Similarity:	99.7%
Query Match:	73.4%
DB:	2

Length:	314
Matches:	313
Conservative:	1
Mismatches:	0
Indels:	0
Gaps:	0

US-09-888-264-1 (1-1123) x Q5RFJ5_PONPY (1-314)

```
Qy        21 ATGGCGGCCGCACGGGCAGTGGCCGGGGCCGGGGATGGACGGGAGAGCCCGTACTCCCCT    80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 MetAlaAlaAlaThrAlaSerAlaAlaGlyAlaGlyMetAspGlyArgGluSerProPro    20

Qy        81 AAGTCCGTCAAGTTCCTGTTTGGGGGCCCTGGCCCGGGGGGCCTGGCAACAGTTTTGTCCAG   140
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        21 LysSerValLysPheLeuPheGlyGlyLeuAlaGlyMetGlyAlaThrValPheValGln    40
```

```
Q5RFJ5_PONPY
ID   Q5RFJ5_PONPY   PRELIMINARY;   PRT;   314 AA.
AC   Q5RFJ5;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Hypothetical protein DKFZp468G0316.
GN   Name=DKFZp468G0316;
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
```

```
Qy        81 AAGTCCGTCAAGTTCCTGTTTGGGGGCCCTGGCCCGGGGGGCCTGGCAACAGTTTTGTCCAG   140
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        21 LysSerValLysPheLeuPheGlyGlyLeuAlaGlyMetGlyAlaThrValPheValGln    40

Qy       141 CCCCTGGACCTGGGTGAAGAACCAGAGTTGACGGGGGAAGGGGCCAAGAGACTCGAGAG   200
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        41 ProLeuAspLeuValLysAsnArgMetGlnLeuSerGlyGluGlyAlaLysArgThrArgGlu    60

Qy       201 TACAAAAACCAGCTTCCATGCCCTCACCAGTATCCTGAAGGCAGAAGGGCCTGAGGGGCATT   260
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 TyrLysThrSerPheHisAlaLeuHisThrSerIleLeuLysAlaGluGlyLeuArgGlyIle    80

Qy       261 TACACTGGGGCGTGCTCGGCCTGGCCTGCGTCGGTCAGGCCACTACCAACTACCCGCCTTGGC   320
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        81 TyrThrGlyLeuSerAlaGlyLeuLeuArgGlnAlaThrTyrThrThrThrArgLeuGly   100

Qy       321 ATCTATACCGGTGCTGTTTGAGCCGCTGACTGGGCGTGATGGTACTCCCCCTGGCTTTCTG   380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       101 IleTyrThrValLeuPheGluArgLeuThrGlyValAlaAspGlyThrProGlyPheLeu   120

Qy       381 CTGAAGGCTGTGATTGGCATGACCACGGCACCACTGGTGCCCTTTGTGGGAACACCAGCC   440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 LeuLysAlaValIleGlyMetThrThrAlaGlyAlaThrGlyValAlaPheValGlyThrProAla   140

Qy       441 GAAGTGGCTCTTATCCGCATGACTGCCGATGGCCGGCTTCCAGCTGACCACCGGCCGTGGC   500
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       141 GluValAlaLeuIleArgMetThrAlaAspGlyArgLeuProAlaAspGlnArgArgGly   160

Qy       501 TACAAAAATGTGTTTAACCCCCTGATTCGAATCACCCGGGAAGAGGGTGTCCTCACACTG   560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       161 TyrLysAsnValPheAsnAlaLeuIleArgIleThrArgGluGluGlyValLeuThrLeu   180

Qy       561 TGGCGCGGGGGCTGCATCCCTACCTACCCATGGACTCGGGGCGTCGTCGTCGTCCCAGCTCGCC   620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 TrpArgGlyGlyCysIleProThrMetAlaArgAlaValValValAsnAlaAlaGlnLeuAla   200
```

OM nucleic - protein search, using frame_plus_n2p model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

Run on: February 1, 2006, 13:33:41 ; Search time 8.25358 Seconds
(without alignments)
2618.292 Million cell updates/sec

Title: US-09-888-264-1
Perfect score: 2181
Sequence: 1 ccgagggccattggatggggcg............ctcattgaggactcaataaa 1123

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
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-DB=PIR -QFMT=fastan -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abss02p
-USER=US09888264 @CGN 1_1_77 @runat_01022006_131840_14810 -NCPU=3 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=10 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_80:*
1: piri:*
2: piri2:*
3: piri3:*
4: piri4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1604	73.5	314	2	A56650	2-oxoglutarate car
2	1549	71.0	314	2	A36305	2-oxoglutarate/mal
3	1052	48.2	323	2	T25459	hypothetical prote
4	602.5	27.6	302	2	S65040	2-oxoglutarate/mal
5	598	27.4	302	2	S65042	2-oxoglutarate/mal
6	583	26.7	297	2	T07405	oxoglutarate/malat
7	583	26.7	313	2	D84613	hypothetical prote
8	554	25.4	313	2	T05577	uncoupling protein
9	527.5	24.2	331	2	T51899	probable 2-oxoglut
10	510	23.4	290	2	S44091	oxoglutarate/malat
11	498	22.8	325	2	JC7553	brain mitochondria
12	468	21.5	325	2	H86274	F7A19.22 protein -
13	459.5	21.1	298	2	S51351	hypothetical prote
14	445.5	20.4	282	2	T49628	probable dicarboxy
15	438.5	20.1	307	2	G01858	uncoupling protein
16	435.5	20.0	306	2	T07793	uncoupling protein
17	426	19.5	312	2	JC5522	uncoupling protein
18	422.5	19.4	307	2	A26294	uncoupling protein
19	415.5	19.1	307	2	A31106	mitochondrial uno
20	415.5	19.1	307	2	S34268	uncoupling protein
21	412	18.9	320	2	T37603	probable oxaloacet
22	411.5	18.9	306	2	T47570	uncoupling protein
23	402.5	18.5	306	2	T52024	uncoupling protein
24	401	18.4	306	2	A32446	uncoupling protein
25	365	16.7	288	2	S03603	mitochondrial unco
26	357.5	16.4	324	2	S25357	hypothetical prote
27	331	15.2	343	2	T15253	probable carrier p
28	305	14.0	322	2	S57116	probable phosphate
29	280.5	12.9	307	2	S60949	hypothetical prote
30	268	12.3	309	2	T48156	hypothetical prote
31	267.5	12.3	702	2	T16533	hypothetical prote
32	257	11.8	392	2	T05350	adenylate transloc
33	253.5	11.6	310	2	S69050	probable membrane
34	245.5	11.3	352	2	T01729	mitochondrial solu
35	233.5	10.7	331	2	F84823	probable peroxisom
36	232	10.6	475	2	T50686	peroxisomal Ca-dep
37	228.5	10.5	299	2	S36081	probable carrier p
38	228	10.5	299	2	S44554	citrate transport
39	227.5	10.4	358	2	T09109	envelope protein t
40	224.5	10.3	335	2	S04453	hypothetical prote
41	224.5	10.3	436	2	JQ1459	Bt1 protein precur
42	223.5	10.2	415	2	T48171	hypothetical prote
43	223	10.2	902	2	S54495	probable carrier P
44	221	10.1	291	2	T37992	probable tricarbox
45	220.5	10.1	311	2	G01789	citrate transporte

RESULT 1

A56650

2-oxoglutarate carrier protein - human
C;Species: Homo sapiens (man)
C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: A56650; S29598
R;Iacobazzi, V.; Palmieri, F.; Runswick, M.J.; Walker, J.E.
DNA Seq., 3, 79-88, 1992
A;Title: Sequences of the human and bovine genes for the mitochondrial 2-oxoglutarate ca
A;Reference number: A56650; MUID:93091249; PMID:1457818
A;Accession: A56650
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-314 <IAC>
A;Cross-references: UNIPROT:Q02978; UNIPARC:UPI000016A206; EMBL:X66114; NID:g923843; PIDN
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: duplication; mitochondrion; transmembrane protein
A;Note: sequence extracted from NCBI backbone (NCBIP:120085)
C;Genetics:
A;Introns: 32/2; 83/2; 152/2; 182/3; 246/2; 263/3
C;Superfamily: ADP,ATP carrier protein
F;18-109/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;116-209/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;216-307/Domain: ADP,ATP carrier protein repeat homology <ACP3>

ALIGNMENTS

Alignment Scores:
Pred. No.: 3.72e-113   Length: 314
Score: 1604.00   Matches: 314
Percent Similarity: 100.0%   Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 73.5%   Indels: 0
DB: 2   Gaps: 0

US-09-888-264-1 (1-1123) x A56650 (1-314)

```
Qy   21 ATGGCGGCGGACGGCGAGTGCCGGGGCGGGGGGGATGGACGGGAAGAGCCCCGTACTCCCT  80
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MetAlaAlaThrAlaSerAlaGlyAlaGlyYGlyMetAspGlyLysProArgThrSerPro  20
```

```
Qy          81 AAGTCCGTCAAGTTCCTGTTTGGGGGCCTGGCGGGGATGGGAGCTACAGTTTTTGTCCAG 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          21 LysSerValLysPheLeuPheGlyGlyLeuAlaGlyMetGlyAlaThrValPheValGln 40

Qy         141 CCCCTGGACCTGGTGAAGAACCGGATGCAGTTCGAGCGCGGGGGAAAGGGGGCCAAGACTCGAGAG 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          41 ProLeuAspLeuValLysAsnArgMetGlnLeuGluSerGlyGluGlyAlaLysThrArgGlu 60

Qy         201 TACAAAAACCAGCTTCCATGCCCTCACCAGTATCCTGAAGCAGCAGAAGGCCTGAGGGCATT 260
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 TyrLysThrSerPheHisAlaLeuLeuSerIleLeuGluLysAlaGluGluLeuArgGlyIle 80

Qy         261 TACACTGGGCTGTCGGCCGTTGGCCTGTGGGTCAGGCGCCACCTACCACCACTACCCCCTGGC 320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          81 TyrThrGlyLeuSerAlaGlyLeuLeuArgGlnIleAlaThrTyrThrThrArgLeuGly 100

Qy         321 ATCTATACCGGTGCTTCCATGCCCTGACTGGAGCGGGTACTCCCCCCGTGGCTTTCTG 380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         101 IleTyrThrValLeuPheGluArgGlnHisGlyAlaGlyTyrAlaGlyPheLeu 120

Qy         381 CTGAAGGCTGTGATTGGCCATGACCGGCAGGTGCCACTGGTGCCTTGTGTGGGAACACAGCC 440
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 LeuLysAlaValIleGlyMetThrAlaGlyValAlaThrGlyAlaPheGluValGlyThrProAla 140

Qy         441 GAAGTGGCTCTTATCCGGCATGACTGCCCGGCTTCCACCTGACCAGCCCCGTGGC 500
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         141 GluValAlaLeuIleArgHisThrAlaAspGlnArgLeuProAlaAspGlnProArgGly 160

Qy         501 TACAAAAATGTGTTTAACCCCGATTCGAATCACCCCGGACAGAGGGGTGTCCTTCACACTG 560
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         161 TyrLysAsnValPheAsnAlaLeuIleArgIleThrArgGlnGluGlyValLeuThrLeu 180

Qy         561 TGGCGGGGGCTGCATCCCTACCATGGCTCGGGGCCGTGCGTCGTCAAAGCTGGCCAGCTCGCC 620
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 TrpArgGlyCysIleProThrMetAlaAlaArgAlaValAlaValValAsnAlaAlaGlnLeuAla 200

Qy         621 TCCTACTCCCAATCCAACGAGCAGTTCTTACTGGACTCAGGGTACTTCTCTGACAACACATCCTG 680
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         201 SerTyrSerGlnSerGlyLysGlnPheLeuLeuAspSerGlyTyrPheSerSerAspAsnIleLeu 220

Qy         681 TGCCACTTCGTGCCAGCATGATGAGCGGTGCTCTTGTCACCACTGCTTGCTTCCCATGCCTGTG 740
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         221 CysHisPheCysAlaSerMetIleSerGlyLeuValThrThrAlaAlaSerMetProVal 240

Qy         741 GACATTGCCAAGACCCGAATCCAGAACATGCGGATGATTGATGGGAAGCCGGAATACAAG 800
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Db         241 AspIleAlaLysThrArgIleGlnAsnMetArgMetIleAspGlyLysProGluTyrLys 260

Qy         801 AACGGGCTGGACTGGCTGTTCAAAAGTTGTCCGCTACGAGGGGGCTTCTTCAGCCGTGTGGAAG 860
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Db         261 AsnGlyLeuAspTrpLeuPheLysSerCysProLeuArgGlyGlyPhePheSerArgValTrpLys 280

Qy         861 GGGTTCACGCCGGTACTATGCCCCGGCCCCCACCACGGTCCTCCACCTTCATCTTCTTG 920
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         921 GAGCGAGATGAACAAGGCCTACAAGCGTCTCTTCCTCAGTGGC 962
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Db         301 GluGlnMetAsnLysAlaTyrLysArgLeuPheLeuSerGly 314
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RESULT 2
A36305

A36305
2-oxoglutarate/malate carrier protein, inner mitochondrial membrane - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C;Accession: A36305; B56650; S65731; A54249; S71377; S29597
R;Runswick, M.J.; Walker, J.E.; Bisaccia, F.; Iacobazzi, V.; Palmieri, F.
Biochemistry 29, 11033-11040, 1990
A;Title: Sequence of the bovine 2-oxoglutarate/malate carrier protein: structural relati
A;Reference number: A36305
A;Accession: A36305; MUID:91105033; PMID:2271695
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-314 <RUN>
A;Cross-references: UNIPROT:P22292; UNIPARC:UPI0000167C3C; EMBL:X66115; PIDN:CAA46906.1; PID:g3
R;Iacobazzi, V.; Palmieri, F.; Runswick, M.J.; Walker, J.E.
DNA Seq. 3, 79-88, 1992
A;Title: Sequences of the human and bovine genes for the mitochondrial 2-oxoglutarate cal
A;Reference number: A56650; MUID:93092249; PMID:1457818
A;Accession: B56650
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-314 <IA2>
A;Cross-references: UNIPARC:UPI0000167C3C; GB:M60662; GB:J05296; NID:g16?
A;Note: sequence extracted from NCBI backbone (NCBIN:120086, NCBIP:120087)
R;Bisaccia, F.; Zara, V.; Capobianco, L.; Iacobazzi, V.; Mazzeo, M.; Palmieri, F.
Biochim. Biophys. Acta 1292, 281-288, 1996
A;Title: The formation of a disulfide cross-link between the two subunits demonstrates th
A;Reference number: S65731; MUID:96176856; PMID:8597574
A;Accession: S65731
A;Status: preliminary
A;Molecule type: protein
A;Residues: 148-160 <BIS>
A;Cross-references: UNIPARC:UPI000017A24
R;Bisaccia, F.; Capobianco, L.; Brandolin, G.; Palmieri, F.
Biochemistry 33, 3705-3713, 1994
A;Title: Transmembrane topography of the mitochondrial oxoglutarate carrier assessed by F
A;Reference number: A54249; MUID:94190892; PMID:8142370
A;Accession: A54249
A;Status: preliminary
A;Molecule type: protein
A;Residues: 6-15,23-32,40-49,62-71,104-113,170-179,183-192 <B12>
A;Cross-references: UNIPARC:UPI000017A25; UNIPARC:UPI000017A26; UNIPARC:UPI000017A27;
R;Bisaccia, F.; Capobianco, L.; Mazzeo, M.; Palmieri, F.
FEBS Lett. 392, 54-58, 1996
A;Title: The mitochondrial oxoglutarate carrier protein contains a disulfide bridge betwe
A;Reference number: S71377; MUID:96354876; PMID:8769314
A;Accession: S71377
A;Molecule type: protein
A;Residues: 148-160,189-200 <BIW>
A;Cross-references: UNIPARC:UPI000017A24; UNIPARC:UPI000017A2C
A;Experimental source: heart
C;genetics:
A;Introns: 32/2; 83/2; 246/2; 263/3
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: duplication; mitochondrion; transmembrane protein
F;18-109/Domain: ADP,ATP carrier protein <ACP1>
F;116-209/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;216-307/Domain: ADP,ATP carrier protein repeat homology <ACP3>
F;221-224/Disulfide bonds: #status experimental

US-09-888-264-1 (1-1123) x A36305 (1-314)

Alignment Scores:
Pred. No.:
Score: 5.27e-109   Length: 314
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Percent Similarity: 97.1%   Conservative: 2
Best Local Similarity: 96.5%   Mismatches: 9
Query Match: 71.0%   Indels: 0
DB: 2   Gaps: 0

US-09-888-264-1 (1-1123) x A36305 (1-314)

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Qy          21 ATGGGCGGCGACGGCGGCAGTGCCCGGCGGCGGCGGGGATGGACGGGAAGCCCCCTACCTCCCCT 80
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Qy          81 AAGTCCGTCAAGTTCCTGTTTGGGGGCCTGGCGGGGATGGGAGCTACAGTTTTTGTCCAG 140
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Db          21 LysSerValLysPheLeuPheGlyGlyLeuAlaGlyMetGlyAlaThrValPheValGln 40

Qy         141 CCCCTGGACCTGGTGAAGAACCGGATGCAGTTCGAGCGCGGGGGAAAGGGGGCCAAGACTCGAGAG 200
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Qy         201 TACAAAAACCAGCTTCCATGCCCTCACCAGTATCCTGAAGCAGCAGAAGGCCTGAGGGCATT 260
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Db          61 TyrLysThrSerPheHisAlaLeuLeuSerIleLeuGluLysAlaGluGluLeuArgGlyIle 80
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OM nucleic - protein search, using frame_plus_n2p_model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on: February 1, 2006, 13:19:02 ; Search time 35.8368 Seconds
                                          (without alignments)
                                          2753.720 Million cell updates/sec

Title:
Perfect score: 2181
Sequence: US-09-888-264-1
                1 ccgagggccattgagtggcg..........ctcattgaggactcaataa 1123

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 4886326

Scoring table: BLOSUM62
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                Ygapop   10.0 , Ygapext   0.5
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                Delop   6.0 , Delext   7.0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

Command line parameters:
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-Q=/abss/ABSSWEB_spool/US09888264/runat_01022006_131837_14767/app_query.fasta_1
-DB=A_Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abss02p
-USER=US09888264 @CGN 1.1.476 @runat_01022006_131837_14767 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   A_Geneseq_21.*
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               6: geneseqp2003as:*
               7: geneseqp2003bs:*
               8: geneseqp2004s:*
               9: geneseqp2005s:*

                               SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1604	73.5	314	7	ADJ68692	Human hea
2	1600	73.4	314	7	ABG75060	Human sol
3	1600	73.4	314	7	ADI63106	Human apo
4	1600	73.4	314	7	ADJ71209	Human hea
5	1600	73.4	314	7	ADJ70398	Human hea
6	1600	73.4	314	8	ADQ89940	Antagonis
7	1576	72.3	342	7	ADC31772	Human nov
8	1576	72.3	342	8	ADJ27213	Human TRI
9	1308.5	60.0	263	8	ADJ27204	Human TRI

RESULT 1
ID   ADJ68692
AC   ADJ68692;
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DT   06-MAY-2004 (first entry)
XX
DE   Human heat mitochondrial protein as a therapeutic target SeqID498.
XX
KW   mitochondrial; human; screening assay; diabetes mellitus;
KW   Huntington's disease; osteoarthritis;
KW   Leber's hereditary optic neuropathy; LHON;
KW   mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW   myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW   neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW   osteopathic; ophthalmological; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO200308778-A2.
XX
PD   23-OCT-2003.
XX
PF   04-APR-2003; 2003WO-US010870.
XX
PR   12-APR-2002; 2002US-0372843P.
PR   17-JUN-2002; 2002US-0389987P.
PR   20-SEP-2002; 2002US-04124418P.
XX
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.
XX

                          ALIGNMENTS

ADJ68692 standard; protein; 314 AA.

10	1056	48.4	312	8	Adx97090	Adx97090 Plant ful
11	1052	48.2	323	8	Adn22668	Adn22668 Bacterial
12	944	43.3	314	9	Ady64720	Ady64720 S. manson
13	915.5	42.0	317	8	Abb58008	Abb58008 Drosophil
14	839.5	38.5	311	4	Abb66966	Abb66966 Drosophil
15	782	35.9	301	4	Abb57921	Abb57921 Drosophil
16	782	35.9	301	4	Adq89738	Adq89738 Antagonis
17	773.5	35.5	178	8	Adn33130	Adn33130 Human tra
18	606	27.8	306	7	Abm73602	Abm73602 Human un
19	602	27.6	344	8	Adx78358	Adx78358 DNA clone
20	597.5	27.4	349	8	Adx78463	Adx78463 Plant ful
21	592	27.1	305	8	Ady07225	Ady07225 Arabidops
22	591	27.1	298	3	Aag09948	Aag09948 Arabidops
23	589	27.0	341	8	Adx89570	Adx89570 Plant ful
24	585.5	26.8	285	8	Adx72228	Adx72228 Plant ful
25	583	26.7	313	3	Aag50517	Aag50517 Arabidops
26	579	26.5	313	3	Aag19643	Aag19643 Arabidops
27	568.5	26.1	273	3	Aag09949	Aag09949 Arabidops
28	554	25.4	313	3	Aag49736	Aag49736 Arabidops
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31	554	25.4	342	3	Aag29873	Aag29873 Arabidops
32	537.5	24.6	262	3	Aag09950	Aag09950 Arabidops
33	535	24.5	284	3	Aag50518	Aag50518 Arabidops
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35	525	24.1	276	8	Ads23506	Ads23506 Bacterial
36	516.5	23.7	272	8	Adn20798	Adn20798 Bacterial
37	513.5	23.5	237	3	Aag50519	Aag50519 Arabidops
38	513.5	23.5	290	8	Adn24153	Adn24153 Bacterial
39	510	23.4	237	3	Aag19645	Aag19645 Arabidops
40	509.5	23.4	302	4	Aam41612	Aam41612 Human pol
41	507	23.2	325	3	Aay94669	Aay94669 Murine un
42	506	23.2	322	3	Aay94668	Aay94668 Murine un
43	505	23.1	280	4	Abb65868	Abb65868 Drosophil
44	504.5	23.1	280	4	Abb71693	Abb71693 Drosophil
45	503.5	23.1	287	4	Aam93644	Aam93644 Human pol

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PI   Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI   Warnock DE;
XX
DR   WPI; 2003-845369/78.
XX
PT   Identifying a mitochondrial target for drug screening assays and for
PT   treating diseases associated with altered mitochondrial function,
PT   comprises detecting a modified polypeptide in a sample and correlating
PT   with the disease.
XX
PS   Claim 1; SEQ ID NO 498; 180pp; English.
XX
CC   This invention relates to novel mitochondrial targets that can be used
CC   for therapeutic intervention in treating a disease associated with
CC   altered mitochondrial function. Specifically, it refers to a method for
CC   identifying proteins of the human heart mitochondrial proteome that are
CC   useful for drug screening assays, as well as therapeutic targets. The
CC   present invention describes a method for identifying such proteins that
CC   can be used in the treatment of various diseases associated with altered
CC   mitochondrial function including diabetes mellitus, Huntington's disease,
CC   osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC   encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC   ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC   compositions have neuroprotective, nootropic, antidiabetic,
CC   anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC   cytostatic activities. This polypeptide sequence is a human heart
CC   mitochondrial protein of the invention.
XX
SQ   Sequence 314 AA;
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US-09-888-264-1 (1-1123) x ADJ68692 (1-314)

  Alignment Scores:
    Pred. No.:
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    Query Match:          100.0%           Conservative:  0
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                                           Indels:        0
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Qy   21 ATGGCGGCGGCACGGCGGCGAGTGCCCGGGCCGGGGATGACGGGGAGGCCCGTACTTCCCT 80
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Qy   81 AAGTCCGTCAAGTTCCTGTTGTTGGGGGGCCCTGGCCCGGGAGAGCTACAGTTTTTTGTCCAG 140
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Db   21 LysSerValLysPheLeuLeuPheGlyGlyLeuAlaGlyMetGlyAlaThrValPheValGln 40

Qy  141 CCCCTGGACCTGTGTGAAGAACCGGATGCAGTTGAGGGGGGAAGGGGGCCAAGACTCGAGAG 200
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Qy  201 TACAAAACCAGCTTCCATCCCCTTCACCAGTATCCTGAAGGCAGAAGGCCTGAGGGGCATT 260
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Db   61 TyrLysThrSerPheHisAlaLeuThrSerIleLeuLysAlaGluGlyLeuArgGlyIle 80

Qy  261 TACACTGGGCTGTGGGCTGGCCTGCGTCAGGCGCCACCTACACCACTACCGCCCTTGGC 320
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Qy  321 ATCTATACCGTGCTGTGTTTGAGCGCCGCCTGACTGGGGTACTCCCCTGGCTTTCTG 380
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Db  101 IleTyrThrValLeuPheGluArgLeuThrGlyLeuAlaAspGlyTyrProProGlyPheLeu 120

Qy  381 CTGAAGGGCTGTGATTGGCATGACACCGGAGGTGCCACTGGTGCCCTTTGTGGGAACCAGC 440
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Db  121 LeuLysAlaValIleGlyMetThrAlaGlyAlaThrGlyAlaPheValGlyThrProAla 140

Qy  441 GAAGTGGGCTCTTATCCGCATGACTGCCCGATGGGCCGGCCTTCCAGCTGACCAGCGCCGTGGC 500
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Db  141 GluValAlaLeuIleArgMetThrAlaAspGlyArgLeuProAlaAspGlnArgArgGly 160

Qy  501 TACAAAATGTTGTTAACGCCCCTGATTCGAATCACCCCGGAGAAGAGGGTGTTCTCACACTG 560
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Db  161 TyrLysAsnValPheAsnAlaLeuIleArgIleThrArgGluGluArgValPheLeuThrLeu 180
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Qy  561 TGGCGGGGGGGCTGCATCCCTACCCATGGCTCGGGGGGCTCGTCGTGCTCGTCAATGCTGCC 620
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Db  181 TrpArgGlyCysIleProThrMetAlaArgAlaValValValAsnAlaAlaGlnLeuAla 200
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Qy  621 TCCTACTCCCAATCCAAGCAGCTTACTGGGACTTCAGGCTCTACTTCTCTGACACAATCCTG 680
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Db  201 SerTyrSerGlnSerLysGlnLeuThrGlyLeuGlnGlySerTyrPheSerAspAsnIleLeu 220

Qy  681 TGCCACTTCTGTGCCCAGCGATGATCAGGCCGGTCTTCACCACTGCTCCCAATGCCTGTG 740
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Db  221 CysHisPheCysAlaSerMetIleSerGlyleuValThrThrAlaAlaSerMetProVal 240

Qy  741 GACATTGCCAAGACCCGGAATCCAGAACATGCGGATGATTGATGATGGGAGACCGGAATACAAG 800
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Db  241 AspIleAlaLysThrArgIleGlnAsnMetArgMetIleAspAspGlyLysProGluTyrLys 260

Qy  801 AACGGGGCTGGACGTGCGTGTTCAAAGTTGTCCGCTACGAGGGGCTTTTCACCCTGTCGAAG 860
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Db  261 AsnGlyLeuAspValLeuPheLysValValArgTyrGluGlyLeuPhePheSerLeuTrpLys 280

Qy  861 GGCTTCACGCCGTACTATGCCCGCCCCTGGGGCCCCCACACCGTCCTCACCTTCATCTTCTG 920
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Db  281 GlyPheThrProTyrTyrAlaArgLeuGlyProHisThrValLeuThrPheIlePheLeu 300

Qy  921 GAGCAGAGTGAAACAAGGCCTACAACCGTTCTTCCTTCAGTGGC 962
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Db  301 GluGlnMetLysAsnLysAlaTyrLysArgLeuPheLeuSerGly 314
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RESULT 2
ABG75060
ID   ABG75060 standard; protein; 314 AA.
XX
AC   ABG75060;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human solute carrier family 25 member 11 protein.
XX
KW   Energy homeostasis; mouse; metabolism; triglyceride; metabolic disease;
KW   gene therapy; anorectic; immunomodulator; antidiabetic; hypotensive;
KW   cardiant; osteopathic; antilipemic.
XX
OS   Homo sapiens.
XX
CC   WO200307S945-A2.
XX
PN   WO200307S945-A2.
XX
PD   18-SEP-2003.
XX
PF   14-MAR-2003; 2003WO-EP002714.
XX
PR   14-MAR-2002; 2002EP-00005882.
PR   15-MAR-2002; 2002EP-00006012.
PR   20-MAR-2002; 2002EP-00006271.
PR   25-MAR-2002; 2002EP-00006810.
XX
PA   (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
XX
PI   Eulenberg K, Steuernagel A, Haeder T, Broenner G;
XX
DR   WPI; 2003-748334/70.
DR   N-PSDB; ACH00820.
XX
PT   New pharmaceutical composition comprising a nucleic acid molecule
PT   encoding proteins regulating the energy homeostasis and metabolism of
PT   triglycerides useful for detecting or preventing metabolic diseases, e.g.
PT   obesity.
XX
PS   Claim 3; Fig 11C; 140pp; English.
XX
CC   The present invention relates to pharmaceutical compositions comprising
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OM nucleic - nucleic search, using sw model          GenCore version 5.1.7
                                                     Copyright (c) 1993 - 2006 Bioacceleration Ltd.
Run on:       February 2, 2006, 15:49:36 ; Search time 574.757 Seconds
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Perfect score: 1123
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Scoring table: IDENTITY_NUC
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Total number of hits satisfying chosen parameters:  12137058

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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              4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
              5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
              6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	136.2	12.1	987	7	US-10-750-185-57090	Sequence 57090, A
2	136.2	12.1	987	7	US-10-750-623-57090	Sequence 57090, A
3	120	10.7	1339	8	US-11-136-527-3307	Sequence 3307, App
4	102.4	9.1	1180	8	US-11-010-239-108	Sequence 108, Appl
5	102.2	9.1	1646	8	US-11-169-041-97	Sequence 97, Appl
6	92.4	8.2	1575	8	US-11-136-527-2535	Sequence 2535, Ap
7	86	7.7	948	8	US-11-128-061-746	Sequence 746, App
8	86	7.7	948	8	US-11-128-049-746	Sequence 746, App
9	80.8	7.2	1194	8	US-11-136-527-3760	Sequence 3760, Ap
10	80.8	7.2	1194	8	US-11-136-527-7856	Sequence 7856, Ap
11	79.8	7.1	935	8	US-11-128-061-747	Sequence 747, App
12	79.8	7.1	935	8	US-11-128-049-747	Sequence 747, App
13	78.8	7.0	924	8	US-11-128-061-391	Sequence 391, App
14	78.8	7.0	924	8	US-11-128-049-391	Sequence 391, App
15	73.4	6.5	600	8	US-11-128-061-4388	Sequence 4388, Ap
16	73.4	6.5	600	8	US-11-128-049-4388	Sequence 4388, Ap
17	66.8	5.9	816	8	US-11-019-711-25	Sequence 25, Appl
18	64.8	5.8	1572	8	US-11-136-527-160	Sequence 160, Appl
19	47.4	4.2	600	8	US-11-136-527-7403	Sequence 7403, Ap
20	47.4	4.2	1455	8	US-10-947-249-147	Sequence 147, Appl
21	47.2	4.2	600	8	US-11-128-061-4389	Sequence 4389, Ap
22	47.2	4.2	600	8	US-11-128-049-4389	Sequence 4389, Ap
c 23	46.2	4.1	600	8	US-11-136-527-5775	Sequence 5775, Ap
c 24	46.2	4.1	1439	8	US-11-136-527-1679	Sequence 1679, Ap
c 25	45.6	4.1	1044	8	US-11-128-061-109	Sequence 109, App
c 26	45.6	4.1	1044	8	US-11-128-049-109	Sequence 109, App
c 27	41	3.7	4393	8	US-11-145-035-39	Sequence 39, Appl
c 28	40.8	3.6	600	8	US-11-136-527-6631	Sequence 6631, Ap
c 29	40.2	3.6	1164	6	US-10-714-887-175	Sequence 175, App
c 30	39.4	3.5	578	8	US-11-128-061-1433	Sequence 1433, Ap
c 31	39.4	3.5	578	8	US-11-128-049-1433	Sequence 1433, Ap
c 32	39.4	3.5	578	8	US-11-128-061-5075	Sequence 5075, Ap
c 33	39.4	3.5	578	8	US-11-128-049-5075	Sequence 5075, Ap
c 34	38.2	3.4	600	8	US-11-128-061-4033	Sequence 4033, Ap
c 35	38.2	3.4	600	8	US-11-128-049-4033	Sequence 4033, Ap
c 36	37.8	3.4	2286	8	US-11-136-527-231	Sequence 231, App
c 37	37.8	3.3	37500	7	US-10-522-037-1	Sequence 1, Appli
c 38	37.6	3.3	1608	8	US-11-114-906-15	Sequence 15, Appl
c 39	37.6	3.3	1647	8	US-11-114-906-13	Sequence 13, Appl
c 40	37.6	3.3	1947	8	US-11-114-906-11	Sequence 11, Appl
c 41	37.6	3.3	1965	8	US-11-114-906-9	Sequence 9, Appli
c 42	37.6	3.3	2256	8	US-11-114-906-7	Sequence 7, Appli
c 43	37.6	3.3	2295	8	US-11-114-906-5	Sequence 5, Appli
c 44	37.6	3.3	2331	8	US-11-114-906-23	Sequence 23, Appl
c 45	37.6	3.3	2370	8	US-11-114-906-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-10-750-185-57090/c

; Sequence 57090, Application US/10750185
; Publication NO. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57090
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-57090   1986680933603

  Query Match   12.1%; Score 136.2; DB 7; Length 987;
  Best Local Similarity   89.1%;
  Matches 147; Conservative   0; Mismatches   18; Indels   0; Gaps   0;

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Qy    112 CCCGGGATGGGGAGCTACACGTTTTTTGTCAGCCCCCTGGGACCTGGTGAAGAACCGGATGCAGT 171
          ||||| |||||||||||||||||||||||  |  ||||||||||||||||| |||||||||||||
Db    177 CCAGGATGGGGAGCTACACGTTTTTGTGTCAGCCCCTTGGACCTGGGTGAAGAACCGGATGCAGC 118

Qy    172 TGAGCGCGGGAAGGGGGCCAAGACTCCGAGAGTACAAAAACCAGCTTCCATGCCCTCCACCAGTA 231
          |||| | ||||||| |||||||||| | |||||||||||||||||||||||||||| || |||| |
Db    117 TGAGTGGGGGAAGGGAGGCCAAGACACGAGAGTACAAAAACCAGCTTCCATGCCCCTCATCAGCA 58

Qy    232 TCCTGAAGGCAGAAGAGGGCCTGAGGGGGCCATTTACACTGGGCTGTCGG 276
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Db     57 TCCTGAAGGGCAGAAGGGCTTATGGGCAATTTACACCGGGTACTGGG 13
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RESULT 2
US-10-750-623-57090/c

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; Sequence 57090, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57090
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Bovine    1986680933603
US-10-750-623-57090
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Query Match       12.1%;  Score 136.2;  DB 7;  Length 987;
Best Local Similarity   89.1%;  Pred. No. 1.9e-28;
Matches  147;  Conservative  0;  Mismatches  18;  Indels  0;  Gaps  0;
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Db  177 CCAGGATGGGGAGCTTACAGTTTTTTGTCAGCCCCCTTGGAGAGAACCGGATGCAGC 118

Qy  172 TGAGCGGGGAAGGGGGCCCAAGACTCGAGAGTACAAAACCAGCTTCCATGCCTCACCAGTA 231
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RESULT 3
US-11-136-527-3307
; Sequence 3307, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-25
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3307
; LENGTH: 1339
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3307
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Best Local Similarity   48.1%;  Pred. No. 8.1e-24;
Matches  416;  Conservative  0;  Mismatches  430;  Indels  18;  Gaps  2;
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Db  178 GTAAAGTTCCTGGGGGGCCCGGCACTGCAGCCTCGTTTTGCTGATCTCCTCACCTTCCCCCTG 237

Qy  147 GACCTGGTGAAGAACCGGATGCAGCTTGACGCGGGGA------AGGGGCCAAGACTCGAGAG 200
        |||||  |||||||||||  |||| |||  |||||||       ||||||||||||||||||
Db  238 GACACCGCAAGTCCGCCTGCGAGATCCAGAGGGGAGAACCCAGGAGTCCAGAGACGGTGCAG 297
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Qy  201 TACAAAAACCAGCTTCCATGCCTCACCAGTATCCTGAAGGCAGAAAGGCCTGAGAGGGGGCATT 260
Db  298 TACCGCCGGGTGCTCGGGTACCATCCTGACTATGGTGGCACGAGAGGGTCCCGCAGCCCC 357

Qy  261 TACACTGGGCTGTCGGCTGGCCCTGCTGGTGGTCAGGCACTATCACCACTACCCGCCTTGGC 320
Db  358 TACAGCGGGTGGTCGGTGCTGGCCCATCGCAGTGAGTCGGCACGAGAGGTCCCGCAGGCCC 417

Qy  321 ATCATTACCGGTGCTGTGTTTGAGCGGCTGACTGGGGTGACGTACTCCCCCTGGGCTTTCTG 380
Db  418 CTCTACGACTCTGTCAAGCAGTTCTACACCCCCAAAGGAACGGACCACTCCAGCGCGTCGCC 477

Qy  381 CTGAAGGCTGTGATTGGGCATGACGCCCAGGTGCCACTGTGGCCTTTGTGTGGGAACACCAGCC 440
Db  478 ATCAGGATTCTGGGACGTGCCACAGGGAGGCCATGGGCAGTGACCCTGTGCTCAACACCACG 537

Qy  441 GAAGTGGCTCTTATCCGCATGACTGCCGATGGCCGGCTTCCAGCTGACCAGCGCCGTGGC 500
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Qy  501 TACAAAAAATGTGTTTAACGCCCTGATTCGAAATCACCCGGGGGGAAGGAAGGAGAGGGTGTCCTCACACTG 560
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Qy  561 TGGCCGGCGGCTGCATCCCTACCATGGCTCGGGGCGGTGTCGTTCGTTCAATGCTTGCCCCAGCTCACTG 620
Db  658 TGGAAAGGGACTTGGCCCAAACATCACAGAAAACCGCCATTGTCAATTGTGCTGAGATGGTG 717

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Db  718 ACCTATGACATCATCAGAGAGAAGTGCTGGACTCTCACCTGTTCACCGACAACTTCCCC 777

Qy  681 TGCCACTTCGTTGCAGCATGATCAGCGGTGCTTGTGCCTCCATGGCTGCTGTG 740
Db  778 TGTCACTTGTTCTCTGCCCTTGGAGCTGGTTTCTTGGTCCACGGAAGGCCTCCCCAGTG 837

Qy  741 GACAATTGCCAAGAACCCGAATCCAGAACATCGGGATTGATTGAATGGGGAAGCCGGGAAATACAAG 800
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Qy  801 AACGGGCTGGACGTGCGTCGTTCAAAAGTGTCGCTACGAGAGGGCCTTCTTCAGCGTCTGGAAG 860
Db  886 AGCCCCCTACACTGTATGCTGAGGATGGGGCCGCCCAGGGATCCCCAAGAGCCTTCACACAA 945

Qy  861 GGCTTCACCGCCGTACTATGCCCGCCGCCCCACACGGTCCTCCTCTCATCTTCTG 920
Db  946 GGATTCATGCCCTCCTTCTGCGGTCTGGGAACCTGTGATGATGTTTGTAACCTAC 1005

Qy  921 GAGCAGAATGAACAAGGCCTACAAG 944
Db 1006 GAGCAGCTGAAAACGGGCCTTGATG 1029
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RESULT 4
US-11-010-239-108
; Sequence 108, Application US/11010239
; Publication No. US20060015970A1
; GENERAL INFORMATION:
; APPLICANT: Roger PENNELL
; APPLICANT: Jack OKAMURO
; APPLICANT: Richard SCHNEEBERGER
; APPLICANT: Yiwen FANG
; APPLICANT: Shing KWOK
; APPLICANT: Diane JOFUKU
; APPLICANT: Edward A. KIEGLE
; APPLICANT: Jonathan DONSON
; APPLICANT: Nestor APUYA
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR
  MODIFYING PLANT CHARACTERISTICS
; FILE REFERENCE: 2750-1585PUS2
; CURRENT APPLICATION NUMBER: US/11/010,239
; CURRENT FILING DATE: 2004-12-09
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2006, 04:06:54 ; Search time 219.383 Seconds
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Title: US-09-888-264-1
Perfect score: 1123
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Scoring table: IDENTITY NUC
              Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued Patents NA:*
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              2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
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              5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	461.2	41.1	2449	3	US-09-949-016-4067	Sequence 4067, Ap
c 2	269.4	24.0	11073	3	US-09-949-016-15809	Sequence 15809, A
c 3	128.6	11.5	2003	3	US-09-620-312D-874	Sequence 874, App
4	118	10.5	1398	3	US-09-463-239-6	Sequence 6, Appli
5	105.4	9.4	550	3	US-09-669-751-190	Sequence 190, App
6	102.2	9.1	930	3	US-10-001-051B-1	Sequence 1, Appli
7	102.2	9.1	1185	3	US-09-949-016-3539	Sequence 3539, Ap
8	102.2	9.1	1255	2	US-08-518-878B-38	Sequence 38, Appl
9	102.2	9.1	1255	2	US-08-294-522B-38	Sequence 38, Appl
10	102.2	9.1	1255	2	US-08-470-868A-38	Sequence 38, Appl
11	102.2	9.1	1596	2	US-08-807-861A-38	Sequence 38, Appl
12	102.2	9.1	1596	2	US-09-210-681-38	Sequence 38, Appl
13	102.2	9.1	1596	3	US-08-946-719A-38	Sequence 38, Appl
14	102.2	9.1	1596	3	US-09-547-983-38	Sequence 38, Appl
15	102.2	9.1	1949	3	US-08-937-466-3	Sequence 3, Appli
16	102.2	9.1	1949	3	US-09-172-528-3	Sequence 3, Appli
17	102.2	9.1	1949	3	US-09-318-199-3	Sequence 3, Appli
18	102.2	9.1	1949	3	US-09-503-579-3	Sequence 3, Appli
19	100.6	9.0	2782	3	US-08-937-466-1	Sequence 1, Appli
20	100.6	9.0	2782	3	US-09-172-528-1	Sequence 1, Appli
21	100.6	9.0	2782	3	US-09-318-199-1	Sequence 1, Appli
22	100.6	9.0	2782	3	US-09-503-579-1	Sequence 1, Appli
23	98.4	8.8	1777	2	US-08-937-466-5	Sequence 5, Appli
24	98.4	8.8	1777	2	US-09-172-528-5	Sequence 5, Appli
25	98.4	8.8	1777	3	US-09-318-199-5	Sequence 5, Appli
26	98.4	8.8	1777	3	US-09-503-579-5	Sequence 5, Appli
27	97.6	8.7	1231	3	US-09-808-457-1	Sequence 1, Appli
28	97.6	8.7	1231	3	US-09-423-410-3	Sequence 3, Appli
29	97.6	8.7	2705	3	US-09-949-016-2947	Sequence 2947, Ap
30	96	8.5	1192	3	US-09-142-565-1	Sequence 1, Appli
31	95.8	8.5	1351	3	US-09-463-239-27	Sequence 27, Appl
32	92.6	8.2	924	3	US-09-023-655-890	Sequence 890, App
33	92.6	8.2	1154	3	US-09-949-016-4530	Sequence 4530, Ap
34	85.4	7.6	1132	3	US-09-808-457-3	Sequence 3, Appli
35	85.2	7.6	512	3	US-09-423-410-5	Sequence 1014, Ap
35	85.2	7.6	512	3	US-09-702-705-1014	Sequence 1014, Ap
36	85.2	7.6	512	3	US-09-736-457-1014	Sequence 1014, Ap
37	85.2	7.6	512	3	US-09-614-124B-1014	Sequence 1014, Ap
38	85.2	7.6	512	3	US-09-671-325-1014	Sequence 1014, Ap
39	85.2	7.6	512	3	US-09-658-824-1014	Sequence 1014, Ap
40	85.2	7.6	512	3	US-10-017-754-1014	Sequence 1014, Ap
41	85.2	7.6	512	3	US-09-651-563-1014	Sequence 1014, Ap
42	85.2	7.6	512	3	US-09-774-528-412	Sequence 412, App
43	76.6	6.8	1883	3	US-10-120-988-412	Sequence 412, App
44	76.6	6.8	1883	3	US-09-702-705-1376	Sequence 1376, Ap
c 45	67.4	6.0	318	3	US-09-949-016-4067	

ALIGNMENTS

RESULT 1
US-09-949-016-4067/c
; Sequence 4067, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US/09/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4067
; LENGTH: 2449
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4067

Query Match   41.1%; Score 461.2; DB 3; Length 2449;
Best Local Similarity 97.0%; Pred. No. 1.9e-110;
Matches 491; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

Qy   253 GGGGGCAHTTACACTGGGCTGCGGCTGCGTGGGCCTGGCGTCAGGCACCTTACACCACTACCC 312
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Qy   313 GCCTTGGCCATCTATACCGTGCGTGCTGTTTGAGCGCCGCAGGCCTGACTGGGTACTCCCCTG 372
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Qy   373 GCTTTCTGCTGAAGGCTGTGATTGGCATGACCGCAGGTGCCCACTGGTTGCCTTGGCTTGGAA 432
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   386 GCTTTCTGCTGAAGGCTGTGATTGGCATGACCGCACCGCAGATGCCCTTTGTGCAGGGGAA 327

Qy   433 CACCAGCCGGAAGTGGCTCTTATCCGCATGACTGCCGATGGCC-GGCTTCCAGCTGGACCAG 491
          |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db   326 CACCAGCCGAAGTGGCTCTTATCCGCATGACTGCCAGTGGCCTTCCAGCTGGACCAG 267

Qy   492 CGCCGTGGCTACAAAAAATGTGTTTAACGCCCCGATTCGAATCACCCGGAAGAGGGGTCTC 551
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Db  552  CTCACACTGTGGCGGGGCTGCATCCCTACCATCGGCTTCGGCGGCGTCGTCAATGCTGCC  611
Qy  206  CTCACACTGTGGCGGGGCTGCATCCCTACCATGGCTCGGCGGCGTCGTCAATGCTGCC  147

Qy  612  CAGCTCGGCGCCTCCTACTCCCAATCCAAGAGAGTGTTCTTACTGGA-CTTCAGGCTACTCTGA  670
Db  146  CAGCTCGGCGCCTCCTACTCCCAATCCAAGCAGTTCTTACTGGACCCCAGGCTACTTCTCTGA  87

Qy  731  CATGGCCTGTGGGACATTGCCAAGACCC  756
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Db   26  CATGCCTGTGGGACATTGCCAAGACCC  1
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Query Match       24.0%;   Score 269.4;  DB 3;  Length 11073;
Best Local Similarity  81.1%;  Pred. No. 4e-60;
Matches 364;  Conservative  0; Mismatches  1;  Indels  84;  Gaps  1;

Qy  112  CCCGGGATCGGGAGCTACAGTTTTTTGTCAGCCCCTGGGACCTGGTGAAGACCGGATGCAGT  171
Db  3062 CCAGGATCGGGAGCTACAGTTTTGTCCAGCCCCTGGACCTGGTGAAGAACCGGATGCAGT  3003
Qy  172  TGAGCGCGGGAAGGGGCCCAAGACTCGAGAGTACAAAAACCAGCTTCCATGCCCTCACCAGTA  231
Db  3002 TGAGCGGGGGAAGGGGCCCAAGACTCGAGAGTACAAAAACCAGCTTCCATGCCCTCACCAGTA  2943
Qy  232  TCCTGAAGGCAGAAGGCCTGAGGGGCCATTTACACTG------  267
Db  2942 TCCTGAAGGCAGAAGGCCATTTACACTGGGGTAATTGGGGCCTCAGGATGGAGG  2883
Qy  268  ------------------------------  267
Db  2882 GTAGACTGTGGGGTTGGCAGCTTAGACCTTGGCCTGATATGTGACCCCTTCTGCTCCTCTCA  2823
Qy  268  GGCTGTGTCGGGCTGCTCGGTCAGGCCCACTCACCTCACCTACCGCCTTGGCATTCTATA  327
Db  2822 GGCTGTGTCGGGCTGCTCGGTCAGGCCCACTCACACTACACCGCCTTGGCATTCTATA  2763
Qy  328  CCCTGCTCGTTTGAGCGCGCTGACTGGGGGTGATGGTAGGTACTCCCCCTGGCTTTCTGCTGAAGG  387
Db  2762 CCGTGCTCGTTTGAGCGGCCTGACTGGGGGCTGATGGTACTCCCCCTGGCTTTCTGCTGAAGG  2703
Qy  388  CTGTGATTGGGCATGACCCAGGTGCCACTGGCCTTTGTGGGAACACCAGCGCGAAGTGG  447
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Query Match       11.5%;   Score 128.6;  DB 3;  Length 2003;
Best Local Similarity  52.8%;  Pred. No. 1.3e-23;
Matches 278;  Conservative  0; Mismatches 249;  Indels  0;  Gaps  0;

Qy  241  CAGAAGGCCTGAGGGGGCATTTACACTGGGCGTGTCGGCTGCGGCCCCACCT  300
Db  354  CCGACGGGCAATCCTGGCACTCTACAGCGGCCTGAGGCGTGCGACAGATGACCT  413
Qy  301  ACACCAACTACCCCGCCTTGGCATCTATACCGTGCTGTTGAGCGGCGCCTTGGGGCTGATG  360
Db  414  ACTCCCTGACTCGGTTCGCCATCTACGAGACTGTGCGGCGACCGTGTGGGCCAAGGCCAGCC  473
Qy  361  GTACTCCCCCTGGCTTTCTGCTGAAGGCTGTGATTGGCATGACCGACCGCAGCAGTGCCACTGGTG  420
Db  474  AGGGGGCCTCTCCCCTTCCACGAGAAGGTGTTGCTGGGCTCCGTGCGCGGTTTAGCTGGAG  533
Qy  421  CCTTTGTGGGAACACGCGGACCGAAGTGGTCTTCATTCCGGATCGCCGATGGCCCGGCTTC  480
Db  534  GCTTCGTGGGGACACGCCGCCGCGGAGCTTGGTCGAACGTCAGGAATGAGAACGACGTGAAGCTGC  593
Qy  481  CAGCTGACCCAGCGCGCGTGGCTACAAAAAATGTGTTTAACGCCCTGATTCGAATCACCCGG  540
Db  594  CCCAGGGGTCAGCGCGCGCAACTACGCCCATGCGCTGGAACTACGCCGTAGTCGTG  653
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OM nucleic - nucleic search, using sw model

Copyright (c) 1993 - 2006   Bioacceleration Ltd.

GenCore version 5.1.7

Run on: February 2, 2006, 00:52:24 ; Search time 4960.27 Seconds
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Title: US-09-888-264-1
Perfect score: 1123
Sequence: 1 ccgagggccattgagtgggcg............ctcattgaggactcaataaa 1123

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
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              10: gb_gss2:*
              11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	968.6	86.3	1369	4	CR590793	CR590793 full-leng
2	968.6	86.3	1386	4	CR606322	CR606322 full-leng
3	968.6	86.3	1429	4	CR620583	CR620583 full-leng
4	968.6	86.3	1467	4	CR603391	CR603391 full-leng
5	968.6	86.3	1477	4	CR617034	CR617034 full-leng
6	968.6	86.3	1479	4	CR595953	CR595953 full-leng
7	968.6	86.3	1488	4	CR591200	CR591200 full-leng
8	968.6	86.3	1515	4	CR617848	CR617848 full-leng
9	968.6	86.3	1529	4	CR598517	CR598517 full-leng
10	968.6	86.3	1532	4	CR609603	CR609603 full-leng
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15	947.6	84.4	1147	5	BX395987	BX395987 full-leng
16	944.6	84.1	1302	4	CR613107	CR613107 full-leng
17	944.6	84.1	1358	4	CR613104	CR613104 full-leng
18	942.6	83.9	1354	4	CR625556	CR625556 full-leng
19	941.8	83.9	945	10	CR613184	CR613184 full-leng
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21	915.2	81.5	1159	1	BX333400	BX333400
22	908.6	80.9	1090	5	BX363653	BX363653
23	908	80.9	1125	1	AL519985	AL519985
24	902.2	80.3	1174	5	BX424850	BX424850
25	898.6	80.0	1117	5	BX381492	BX381492
26	896	79.8	1087	5	BX463231	BX463231
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28	889.2	79.2	1039	1	AL580443	AL580443
29	888.8	79.1	1165	1	AL547659	AL547659
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31	874.4	77.9	1121	1	AL530824	AL530824
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33	857.6	76.4	1271	4	CR605572	CR605572 full-leng
34	852	75.9	871	1	AL520894	AL520894
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40	813.2	72.4	1061	3	BM921558	BM921558 AGENCOURT
41	813	72.4	850	10	BM924580	BM924580 AGENCOURT
42	812.4	72.3	1003	3	AY415735	AY415735 Pan trogl
43	812	72.3	1055	3	BI757743	BI757743 603029708
44	810.6	72.2	1149	5	BX447797	BX447797
45	809.8	72.1	813	8	DR763694	DR763694 HBSCA_155

ALIGNMENTS

RESULT 1
LOCUS   CR590793   1369 bp   mRNA   linear   HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DC025YC08 of Neuroblastoma Cot
            25-normalized of Homo sapiens (human).
ACCESSION   CR590793
VERSION   CR590793.1 GI:50471600
KEYWORDS   HTC; CNS11_cDNA.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 1369)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK   Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2 (bases 1 to 1369)
  AUTHORS   Genoscope.
  TITLE   Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT   1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES   Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="CS0DC025YC08"
                     /tissue_type="Neuroblastoma Cot 25-normalized"
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ORIGIN

Query Match   86.3%; Score 968.6; DB 4; Length 1369;
Best Local Similarity   99.1%; Pred. No. 1e-240;
Matches 974; Conservative   0; Mismatches   9; Indels   0; Gaps   0;

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Qy      1 CCGAGGGGCCATTGAGTGGGGATGGCGGGAGTGGCGGAGTGGCGGAGTGGCGGAGATGGACG   60
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Db      8 CCGAGGGGCCATTGAGTGGGGATGGCGGGCGGGGCGGGCGGGCGGGGCGGGGGGATGG     67

Qy     61 GGAAGCCCCGTACCTCCCCTAAGTCCGTCAAGTTCCTGTTCTGTTGGGGGGCCCGGGGATGG  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     68 GGAAGCCCCGTACCTCCCCTAAGTCCGTCAAGTTCTCGTTCTGTTGGGGGGCCCGGGGGG   127

Qy    121 GAGCTACACGTTTTTGTCCAGCCCCCTGGACCTGGTGAGAGAACCCGAGTTGAGCGGGGG    180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    128 GAGCTACAGTTTTTTGTCCAGCCCCTGGTTGGCATGCAGTTGAGCGGGGG           187

Qy    181 AAGGGGCCAAGACTCGAGAGTACAAAAACCAGCTTCCATGCCCTCACCAGTATCCTGAAGG  240
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Db    188 AAGGGGCCAAGACTCGAGAGTACAAAAACCAGCTTCCATGCCCTCACCAGTATCCTGAAGG   247

Qy    241 CAGAAGGGCCTGAGGGGCATTTACACTGGGCTTGGTCGGGGGTGGCCTGGGTCAGGCCACCT  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    248 CAGAAGGGCCTGAGGGGCATTTACACTGGGCTTGGTCGGGGGTGGCCTGGGTCAGGCCACCT   307

Qy    301 ACACCACTACCCGCCTTGGCATCTATACCGTGCTGCTTTGGGGGCTGACTGGGCTGATG     360
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Db    308 ACACCACTACCCGCCTTGGCATCTATACCGTGCTGCTTTGGGGGCTGACTGGGCTGATG    367

Qy    361 GTACTCCCCCTGGCTTTTCTGCTGAAAGGGTCGTGAGATGGCATGACCGCGCCGCCTGGTG  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    368 GTACTCCCCCTGGCTTTTCTGCTGAAAGGGTCGTGAGATGGCATGACCGCGCCGCCTGGTG   427

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Db    428 CCTTTGTGGGAACACCAGCCGGGCATTTACACTGGGGCTTCTTATCCGGCCCGATGGGCTTC   487

Qy    481 CAGCTGACCCAGCGCCGTGGGCTACAAAAATGTGTTTAACGGGCCCTGAATCACCCGGG    540
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Db    488 CAGCTGACCCAGCGCCGTGGGCTACAAAAATGTGTTTAACGGGCCCTGAATCACCCGGG   547

Qy    541 AAGAGGGGTGTCTCACACTGTGCGGGGCCTGCCATCCCATGGCTCGGGCGCCGTCG      600
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Qy    601 TCAATGCTGCCCAGCTCGCCTCCTACTCCCAATCCAGCAGTTCTTACTGGACTCAGGCT     660
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Db    608 TCAATGCTGCCCAGCTCGCCTCTACTCCCAATCCAGCAGTTCTTACTGGACTCAGGCT    667

Qy    661 ACTTCTCTGACAACATCCTGTGCCACTTCTGTGCCGCACGATGATGATGACGTCTGTGCACCA  720
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Db    668 ACTTCTCTGACAACATCTTGTGCCACTTCTGTGCCGCAGCATGATCAGCCGGTCTTGTCACCA   727

Qy    721 CTGCTGCCTCCATGCCCTGTGGGACATTGCCAAGACCCGGAATCCAGAAACATCAGAACA   780
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Db    728 CTGCTGCCTCCATGCCCTGTGGGACATTGCCAAGACCCGGAATCCAGAAACATGCGGATGAG   787

Qy    781 ATGGGGAAGGCCGGAATACAAGAACACGGGCTGGACGTGCTGTTCGGGCTACGAGG      840
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Db    788 ATGGGGAAGGCCGGAATACAAGAACACGGGCTGGACGTGCTGTTCCGGGCTACGAGG   847

Qy    841 GCTTCTTCAGCCTGTGGAAGGGGCTTCAGGGGTACGGGGCCCCCACACCG       900
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    848 GCTTCTTCAGCCTGTGGAAGGGGCTTCAGGCCGTACTATGCCCCCCACACCG        907

Qy    901 TCCTCACCTTCACTCTTCTTGGACGAGAGTGAACAAAGGGCCTTACACAAGCGTCTTCTCACTG  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    908 TCCTCACCTTCATCTTCTTGGAGCAGAGTGAACAAGGGCCTCTACAAGCGTCTCCTTCAGTG   967

Qy    961 GCTGAAGGCTTTCAGGGGCCACACA  983
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Db    968 GCTGAAGAGGGGCCGGGGGCTCCCA  990
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Query Match             86.3%;  Score 968.6;  DB 4;  Length 1386;
Best Local Similarity   99.1%;  Pred. No. 1e-240;
Matches  974;  Conservative   0;  Mismatches   9;  Indels   0;  Gaps   0;

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Db     35 CCGAGGGGCCATTGAGTGGGGATGGCGGGCGGGGCGGGCGGGCGGGGCGGGGGGATAGACG   94

Qy     61 GGAAGCCCCGTACCTCCCCTAAGTCCGTCAAGTTCCTGTTCTGTTGGGGGGCCCGGGGATGG  120
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Db     95 GGAAGCCCCGTACCTCCCCTAAGTCCGTCAAGTTCTCGTTCTGTTGGGGGGCCCGGGGGG   154

Qy    121 GAGCTACACGTTTTTGTCCAGCCCCCTGGACCTGGTGAGAGAACCCGAGTTGAGCGGGGG    180
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Qy    181 AAGGGGCCAAGACTCGAGAGTACAAAAACCAGCTTCCATGCCCTCACCAGTATCCTGAAGG  240
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Qy    241 CAGAAGGGCCTGAGGGGCATTTACACTGGGCTTGGTCGGGGGTGGCCTGGGTCAGGCCACCT  300
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Db    275 CAGAAGGGCCTGAGGGGCATTTACACTGGGCTTGGTCGGGGGTGGCCTGGGTCAGGCCACCT   334

Qy    301 ACACCACTACCCGCCTTGGCATCTATACCGTGCTGCTTTGGGGGCTGACTGGGCTGATG     360
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Db    335 ACACCACTACCCGCCTTGGCATCTATACCGTGCTGCTTTGGGGGCTGACTGGGCTGATG    394

Qy    361 GTACTCCCCCTGGCTTTTCTGCTGAAAGGGTCGTGAGATGGCATGACCGCGCCGCCTGGTG  420
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Qy    421 CCTTTGTGGGAACACCAGCCGGGCATTTACACTGGGGCTTCTTATCCGGCCCGATGGGCTTC  480
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Db    455 CCTTTGTGGGAACACCAGCCGGGCATTTACACTGGGGCTTCTTATCCGGCCCGATGGGCTTC   514
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                    GenCore version 5.1.7
          Copyright (c) 1993 - 2006  Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:        February 2, 2006, 04:06:54 ; Search time 293.617 Seconds
                                            (without alignments)
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Title:         US-09-888-264-2
Perfect score: 1503
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Scoring table: IDENTITY_NUC
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Searched:      1303057 seqs, 888780828 residues
Total number of hits satisfying chosen parameters:    2606114

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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c 2	497	33.1	2449	3	US-09-949-016-4067	Sequence 4067, App
c 3	130.2	8.7	2003	3	US-09-620-312D-874	Sequence 874, App
4	118	7.9	1398	3	US-09-463-239-6	Sequence 6, Appli
5	105.4	7.0	550	3	US-09-669-751-190	Sequence 190, App
6	100.6	6.7	930	3	US-10-001-051B-1	Sequence 1, Appli
7	100.6	6.7	1185	3	US-09-949-016-3539	Sequence 3539, Ap
8	100.6	6.7	1255	2	US-08-518-878B-38	Sequence 38, Appl
9	100.6	6.7	1255	2	US-08-294-522B-38	Sequence 38, Appl
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12	100.6	6.7	1596	2	US-08-807-861A-38	Sequence 38, Appl
13	100.6	6.7	1596	3	US-08-946-719A-38	Sequence 38, Appl
14	100.6	6.7	1596	3	US-09-547-983-38	Sequence 38, Appl
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45	66.8	4.4	816	3	US-10-037-417-25	Sequence 25, Appl

ALIGNMENTS

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RESULT 1
US-09-949-016-15809/c
; Sequence 15809, Application US/0994901
; Patent No. 6812339
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR FILING DATE: 2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15809
;   LENGTH: 11073
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-15809

Query Match             39.9%;  Score 600.4;  DB 3;  Length 11073;
Best Local Similarity   67.2%;  Pred. No. 1.4e-142;
Matches 1286; Conservative 0; Mismatches 6; Indels 622; Gaps 6;

Qy          203 CCGGGATGGGAGCTCACAGTTTTTTGTCCAGCCCCTGGACCTGGTGAAGAAACCGGATGCGT 262
                |  ||||||||||||||||||||||||| ||||||||||||||||||| ||||||||||
Db         3062 CCAGGATCGGAGCTACAGTTTTTTGTCCAGCCCCTGGACCTGGTGAAGAACCCGGATGCAGT 3003

Qy          263 TGAGCGCGGGAAGGGGCCAAGGACTTCGAGAGTACAAAAACCAGCTTCCATGCCCTCACCAGTA 322
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3002 TGAGCGCGGGAAGGGGCCAAGGACTTCGAGAGTACAAAAACCAGCTTCCATGCCCTCACCAGTA 2943

Qy          323 TCCTGAAGGCAGAAGGGCCTGAGGGGGCATTACACTG----- 358
                ||||||||||||||||||||||||||||||||||||
Db         2942 TCCTGAAGGCAGAAGGGCCTGAGGGGGCATTTACACTGGGTATTGGGGGCCTCAGGATGGGAGG 2883

Qy          359 -----------------------------------------  358
Db         2882 GTAGACTGTGGGTTGGCAGCTCTTAGACCTTGGCCTGATTATGCTGACCCCTCTGCTCCTCA 2823

Qy          359 GGCTGTTCGGCCTGCCTCGTGCCTCAGGCCCACCTTACACCACTACCGCCTTGGCATCTATA 418
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db              ...
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RESULT 2
US-09-949-016-4067/c
Sequence 4067, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4067
LENGTH: 2449
TYPE: DNA
ORGANISM: Human
US-09-949-016-4067

Query Match   33.1%; Score 497; DB 3; Length 2449;
Best Local Similarity   81.3%; Pred No. 1.7e-116;
Matches   682; Conservative 0; Mismatches 5; Indels 152; Gaps 3;

(Page consists of DNA sequence alignment rows labeled Qy/Db with nucleotide sequences and positional numbering.)

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OM nucleic - nucleic search, using sw model

                    GenCore version 5.1.7
                    Copyright (c) 1993 - 2006 Biocceleration Ltd.

Run on:          February 2, 2006, 15:49:36 ; Search time 769.243 Seconds
                                            (without alignments)
                                            1637.486 Million cell updates/sec

Title:           US-09-888-264-2
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Scoring table:   1
Scoring table:   IDENTITY NUC
                 Gapop 10.0 , Gapext 1.0
Searched:        6068529 seqs, 419036697 residues
Total number of hits satisfying chosen parameters:      12137058

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_NA_New:*
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                 7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
                 8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
                 9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
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                 11: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

                 Pred. No. is the number of results predicted by chance to have a
                 score greater than or equal to the score of the result being printed,
                 and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	165.8	11.0	987	7	US-10-750-185-57090	Sequence 57090, A
c 2	165.8	11.0	987	7	US-10-750-623-57090	Sequence 57090, A
c 3	118.4	7.9	1339	8	US-11-136-527-3307	Sequence 3307, Ap
4	102.4	6.8	1180	8	US-11-010-239-108	Sequence 108, App
5	100.6	6.7	1646	8	US-11-169-041-97	Sequence 97, Appl
6	90.8	6.0	1575	8	US-11-136-527-2535	Sequence 2535, Ap
7	84.4	5.6	948	8	US-11-128-061-746	Sequence 746, App
8	84.4	5.6	948	8	US-11-128-049-746	Sequence 746, App
9	79.2	5.3	1194	8	US-11-136-527-3760	Sequence 3760, Ap
10	79.2	5.3	1194	8	US-11-136-527-7856	Sequence 7856, Ap
11	78.2	5.2	935	8	US-11-128-061-747	Sequence 747, App
12	78.2	5.2	935	8	US-11-128-049-747	Sequence 747, App
13	77.2	5.1	924	8	US-11-128-061-391	Sequence 391, App
14	77.2	5.1	924	8	US-11-128-049-391	Sequence 391, App
15	71.8	4.8	600	8	US-11-128-061-4388	Sequence 4388, Ap
16	71.8	4.8	600	8	US-11-128-049-4388	Sequence 4388, Ap
17	66.8	4.4	816	8	US-11-019-711-25	Sequence 25, Appl
18	66.4	4.4	1572	8	US-11-136-527-160	Sequence 160, App
19	49	3.3	1455	7	US-10-947-249-147	Sequence 147, App
20	47.2	3.1	1044	8	US-11-128-061-109	Sequence 109, App
21	47.2	3.1	1044	8	US-11-128-049-109	Sequence 109, App
c 22	46.8	3.1	600	8	US-11-136-527-5775	Sequence 5775, Ap
23	46.8	3.1	1439	8	US-11-136-527-1679	Sequence 1679, Ap
24	45.8	3.0	600	8	US-11-136-527-7403	Sequence 7403, Ap
25	45.6	3.0	600	8	US-11-128-061-4389	Sequence 4389, Ap
26	45.6	3.0	600	8	US-11-128-049-4389	Sequence 4389, Ap
27	43	2.9	4393	8	US-11-145-035-39	Sequence 39, Appl
28	42.2	2.8	1271	8	US-11-024-959-68	Sequence 68, Appl
c 29	41	2.7	4950	7	US-11-775-169-157	Sequence 157, App
c 30	40.8	2.7	1264	8	US-11-136-527-6631	Sequence 6631, Ap
31	40.6	2.7	1264	6	US-11-024-959-69	Sequence 69, Appl
32	40.2	2.7	1164	8	US-11-714-887-175	Sequence 175, App
33	39.6	2.6	5300	8	US-11-000-688-563	Sequence 563, App
34	39.4	2.6	578	8	US-11-128-061-1433	Sequence 1433, Ap
35	39.4	2.6	578	8	US-11-128-049-5075	Sequence 5075, Ap
36	39.4	2.6	578	8	US-11-128-061-5075	Sequence 5075, Ap
37	39.4	2.6	1608	8	US-11-114-906-15	Sequence 15, Appl
38	39.2	2.6	1647	8	US-11-114-906-13	Sequence 13, Appl
39	39.2	2.6	1947	8	US-11-114-906-9	Sequence 9, Appli
40	39.2	2.6	1965	8	US-11-114-906-11	Sequence 11, Appl
41	39.2	2.6	2256	8	US-11-128-049-1433	Sequence 1433, Ap
42	39.2	2.6	2256	8	US-11-114-906-7	Sequence 7, Appli
43	39.2	2.6	2295	8	US-11-114-906-5	Sequence 5, Appli
44	39.2	2.6	2331	8	US-11-114-906-23	Sequence 23, Appl
45	39.2	2.6	2370	8	US-11-114-906-21	Sequence 21, Appl

ALIGNMENTS

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RESULT 1
US-10-750-185-57090/c
Sequence 57090, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57090
;  LENGTH: 987
;  TYPE: DNA
;  ORGANISM: Bovine   1986680933603
US-10-750-185-57090

Query Match             11.0%;  Score 165.8;  DB 7;  Length 987;
Best Local Similarity   93.4%;  Pred. No. 1.5e-32;
Matches  184;  Conservative  0;  Mismatches  12;  Indels  1;  Gaps  1;

Qy     12 GGGTGCCGCGCGCGCCCTCG-CTCTGTTGCGCGCGCGGTGTCACTTGGGTGGGCGGGGCC 70
          |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db    964 GTGCGCGCGGCGGCGCCCTCGCCCCCTCGTTGCGCGCGGCGCGGGGTGTCACTTGGGTGGGCGGGGCC 905

Qy     71 GTGCGCGCGCACGGGACCCCGGAGCGCCGAGGGCCATTGAGTGGCGCAGCGGGACGGGAGTG 130
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    904 GCGCGCGCGCACGGGACCCGAGCGCCGAGGGCCATTGAGTGGCGCAGCGGGACGGGAGTC 845

Qy    131 CCGGGCCGCGGCGGGGGGATAGCACGGGAAGAAGCCCCGTACCTCCCCTAAGTCGGTTCCTTGT 190
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    844 CCGGGGCTTCTGGGATGACGGGAAGAAGCCCCGTACCTCCCCTAAGTCCCGTCAAGTTCCTGT 785

Qy    191 TTGGGGGGCCTGGCCGCGGG 207
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Db    784 TTGGGGGGCCTGGCCGGG 768
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RESULT 2
US-10-750-623-57090/c
Sequence 57090, Application US/10750623
Publication No. US20050287531A1
GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 57090
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-623-57090 1986680933603

Query Match 11.0%; Score 165.8; DB 7; Length 987;
Best Local Similarity 93.4%; Pred. No. 1.5e-32;
Matches 184; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy   12 GCGGTGCGCGGCGCGCCCTCG-CTCTCGTTGCGGCGGGCGGGTCACCTTGGGCGTGGGGCGGGGGCC   70
          ||||||||| |||||| |||| |||||||| ||||||||||| |||| ||||||||| ||||||||
Db   964 GTCGCGCGGCGCGCCCTCGCGCCCCTCGTTGCGCGGCGGGCGGTCACCTTGGGCGCGGGACGGGGGCC   905

Qy   71 GTGCGCGGCCACGGGACACCCGGACCGGAGGGGCCCATTGAGTGGGTGGCGATGGTGGGGCGGGAGTG   130
          |||||||| || ||||||||| |||||||||||||||||||||| ||||||||| |||||||||||||
Db   904 GCGCGCGCCACGGGACACCCGGACCGGAGGGGCCCATTGAGTGGGTGGCGATGGTGGGGCGGGAGTC   845

Qy   131 CCGGGGGCCGGCGGCGGGATAGACAGGGAAAGCCCCGTACCTCCCCTAAGTCGCCTCAAGTTCCTGT   190
          ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   844 CCGGGGCGTTCTGGGATGGACAGGGAAAGCCCCGTACCTCCCCTAAGTCGCCTCAAGTTCCTGT   785

Qy   191 TTGGGGGGGCCTGGCCGCGGG   207
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RESULT 3
US-11-136-527-3307
Sequence 3307, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3307
; LENGTH: 1339
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3307

Query Match 7.9%; Score 118.4; DB 8; Length 1339;
Best Local Similarity 48.0%; Pred. No. 2e-20;
Matches 415; Conservative 0; Mismatches 431; Indels 18; Gaps 2;

Qy   178 GTCAAGTTCCTGTTTGGGGGGCCTGGCCCGGGATGGGAGTCTACAGTTTTTGTCCAGCCCCTG   237
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Db   178 GTAAAGTTCCTGGGGGGCCGGGCACTGCAGCCTGTTTTGTGATCTCCTCACCTTCCCCTG   237

Qy   238 GACACCCGCAAGGTCCGCCTGCAGATCCAAGGCAGGAGAACCCAGAGAGTGCAGAGGCTGCAG   297
          ||| || ||| ||| || || |||||| | |||||||||| || ||| |||
Db   238 GACCTGGTGAAGAACCGGATGCAGTTGAGCGGGGA------AGGGCCAAGACTCGAGAG   291

Qy   298 TACCGGCGGGGTGTCGTGGCTCGGGTACCATCCTGACTATGGTGCCGACAGAGGGGTCCCCGCCCGGAGCCCC   357
          ||||||||| || | || |||| | || || ||| |||||| | ||| | ||||| |||||||||
Db   292 TACAAAACCAGCTTCCATGCCCTCACCAGTATCCTGAAGGCAGCAGAAGGCATT   351

Qy   352 TACACTGGGCTGTCGGCCTGGCCTTGGCTTCAGCGCCACCTACACCACTACCCGGCCTTGGC   411
          |||| || ||| || | || ||| |||||||| | |||| || ||| || ||
Db   352 TACCGGCGGGTGCTCGGGTACCATCCTGACTATGGTGCCGACAGAGGGGTCCCCGCCCGGAGCCCC   417

Qy   412 ATCTATACCGTGCTGTTGAGCGCCTGACTGGGGGCTGAGGGTACTCCCCGTCGGCTTTCTG   471
          ||| || || || ||| || ||||| | || | || || | ||| |
Db   418 CTCTACGACTCTGTCAAGCAGTTCTACACCCCCAAAAGAAGAACGGAACCACTCCAGCGTCGCC   477

Qy   472 CTGAAGGCTGTGATTGGCATGACGGCAGTTGCCACTGGTGCCCTTTGTGGGAAACACCAGCC   531
          |||| | |||| ||| ||||| | || || || || | | | || | |||
Db   478 ATCAGGATTCGTGGCCAGGGGCTGCACCCACGGGAGACGCCAGTGACCTGGTCTCAACCCACG   537

Qy   532 GAAGTAGGCTCTTATCCCGATGACTGCCCGATGGCCGGGCGGCTTCCAGCTGACCAGCGCCGTGGC   591
          |||||||| | |||||| |||| |||||||||| | |||| ||||| | || ||
Db   538 GATGTGGTGAAAGTCCGATTTCAAGCCATGAATACGGCCTCGGGACTGGAGACGGAGAGGAAA   597

Qy   592 TACAAAAAATGTGTTTAACGCCCTGATTCGAAATCACCCGGGAAGCAGGGGGTCCTCCACACTG   651
          |||| | |||| | || || ||||||| | ||| | |||||| ||| || | ||
Db   598 TACAGAGGGACTAATGGATGCCTACAGGACCATCGCCGAGAAGAAAGGAGTCAGGGGACTG   657

Qy   652 TGGCGGGGGCTGCATCCCTACCCATGGCCTCGGGCGCGCGTCGTCGTCAATGCTGCCCAGCTCGCC   711
          ||||||| || | || || | || | ||| | | | || || |||||| | || ||||
Db   658 TGGAAAGGGACTTGGCCCCAACATCACAACAGAAACCGCCATTGTCAATTGTGCTGAGATGTGTG   717

Qy   712 TCCTTACTCCCAATCCAAGCACAGTTCTTACTGGACTTGCAGGGTCAGGGTACTTCTCTGACACACATCTTG   771
          | || | | || ||||| || || |||| || || || || || | |
Db   718 ACTTATGACATCAACAAGAGAGAAGCCTGTTGGACTCTCACCTGTTCACTGACAACTTCCCC   777

Qy   772 TGCCACTTCTGTGCCAGCATGACTGGGTCTTGTTCACCAACTGCCCTCCATGCCTGTG   831
          ||| | || ||||| ||||| |||| || | || || || | || || ||
Db   778 TGTCACTTTGTCTCTGCCTTTGGAGCTGTTTCTGTGCCACGGTGGTGGCCACGGTG   837

Qy   832 GACATTGCCAAGACCCGAAATCAGAAACATGCGGAATGATTGATTGGGGAAGCCGGGAATACAAG   891
          ||| | ||| | | || | || || ||||| || ||| | | ||||
Db   838 GATGTGGTAAAGAACCCGATAC-----------ATGAACGCTCCCCCAGGCAGGCAGGTACCGA   885

Qy   892 AACGGGGCTGGGACCTGGCTGCTGGTTCAAAGTTGTCCGGCTACGGAGGGGCTTCTTCAGCCTGGAAG   951
          || ||| || || || || ||||| | || || ||||||||||| | ||| ||||| | |
Db   886 AGCCCCTACACTGTATCGTGAGGAGGGCCCCAGCGGCCCCACAGCCTTCTACAA   945

Qy   952 GGCTTCACGCGTACTATGCCCGGCTGGGCCCCCACACCGTCTCACCTTCATCTTCTG   1011
          ||||||||| | || || || || ||| ||| | | | || || ||||||
Db   946 GGATTCATGCCCTCCTTCTGGGATCCTGGACGTGATGATGTTTGTAACCTAC   1005

Qy   1012 GAGCAGAGTGAACAAAGGCCTTACAAG   1035
          ||||||| ||| | |||| |||
Db   1006 GAGCAGCTGAAAACGGGCCTTGATG   1029

RESULT 4
US-11-010-239-108
Sequence 108, Application US/11010239
Publication No. US20060015970A1
GENERAL INFORMATION:
; APPLICANT: Roger PENNELL
; APPLICANT: Jack OKAMURO
; APPLICANT: Richard SCHNEEBERGER
; APPLICANT: Yiwen FANG
; APPLICANT: Shing KWOK
; APPLICANT: Diane JOFUKU

OM nucleic - protein search, using frame plus n2p model

Copyright (c) 1993 - 2006 Biocceleration Ltd.
GenCore version 5.1.7

Run on: February 1, 2006, 13:19:02 ; Search time 47.9632 Seconds
(without alignments)
2753.720 Million cell updates/sec

Title: US-09-888-264-2
Perfect score: 2847
Sequence: 1 cctcgtgcaggcgtcgcg..........ccaaaaaaaaaaaaaaaaaaa 1503

Searched: 2443163 seqs, 439378781 residues

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Total number of hits satisfying chosen parameters: 4886326

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Command line parameters:
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-DB=A_Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abss02p
-USER=US0988264 @CGN 1 1_476 @runat_01022006_131837_14767 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=10 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_21:*
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7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%	Query Match Length	DB	ID	Description
1	1603	56.3	314	7	ABG75060	Abg75060 Human sol
2	1603	56.3	314	7	ADI63106	Adi63106 Human apo
3	1603	56.3	314	7	ADY64720	Ady64720 Human hea
4	1603	56.3	314	7	ADJ71209	Adj71209 Human hea
5	1603	56.3	314	7	ADJ70398	Adj70398 Human hea
6	1600	56.2	314	7	ADQ89940	Adq89940 Antagonis
7	1579	55.5	342	7	ADJ68692	Adj68692 Human hea
8	1579	55.5	342	8	ADC31772	Adc31772 Human nov
9	1311.5	46.1	263	8	ADJ27204	Adj27204 Human TRI
10	1060	37.2	312	8	Adx97090	Adx97090 Plant ful
11	1058.5	37.2	323	8	Adn22668	Adn22668 Bacterial
12	946	33.2	314	9	Ady64720	Ady64720 S. manson
13	919.5	32.3	317	8	Abb58008	Abb58008 Drosophil
14	840.5	29.5	311	4	Abb66966	Abb66966 Drosophil
15	781	27.4	301	4	Abb57921	Abb57921 Drosophil
16	781	27.4	301	8	Adq89738	Adq89738 Antagonis
17	776.5	27.3	178	8	Adn33130	Adn33130 Human tra
18	606	21.3	306	7	Abm73602	Abm73602 Human tra
19	603.5	21.2	344	8	Adx78358	Adx78358 Plant ful
20	602.5	21.2	349	8	Adx78463	Adx78463 Plant ful
21	592.5	20.8	305	8	Ady07225	Ady07225 Plant ful
22	591	20.7	298	8	Aag09948	Aag09948 Arabidops
23	589	20.7	341	8	Adx89570	Adx89570 Plant ful
24	585.5	20.6	285	8	Adx72228	Adx72228 Plant ful
25	583	20.5	313	8	Aag50517	Aag50517 Arabidops
26	579	20.3	313	8	Aag19643	Aag19643 Arabidops
27	568.5	20.0	273	8	Aag09949	Aag09949 Arabidops
28	554	19.5	313	8	Aag49736	Aag49736 Arabidops
29	554	19.5	313	8	Aag29874	Aag29874 Arabidops
30	554	19.5	341	8	Aag49735	Aag49735 Arabidops
31	554	19.5	342	8	Aag29873	Aag29873 Arabidops
32	537.5	18.9	262	8	Aag09950	Aag09950 Arabidops
33	535	18.8	284	8	Aag50518	Aag50518 Arabidops
34	531	18.7	284	8	Aag19644	Aag19644 Arabidops
35	525	18.4	276	8	Ads23506	Ads23506 Bacterial
36	516.5	18.1	272	8	Adn20798	Adn20798 Bacterial
37	513.5	18.0	237	8	Aag50519	Aag50519 Arabidops
38	510	18.0	290	8	Adn24153	Adn24153 Bacterial
39	509	17.9	237	3	Aag19645	Aag19645 Arabidops
40	507.5	17.8	302	4	Aam41612	Aam41612 Human pol
41	506	17.8	325	3	Aay94669	Aay94669 Murine un
42	505	17.7	322	3	Aay94668	Aay94668 Murine un
43	504.5	17.7	280	4	Abb65868	Abb65868 Drosophil
44	504.5	17.7	280	8	Abb71693	Abb71693 Drosophil
45	503.5	17.7	287	4	Aam93644	Aam93644 Human pol

ALIGNMENTS

RESULT 1
ABG75060
ID   ABG75060 standard; protein; 314 AA.
XX
AC   ABG75060;
XX
DT   12-FEB-2004 (first entry)
XX
DE   Human solute carrier family 25 member 11 protein.
XX
KW   Energy homeostasis; mouse; metabolism; triglyceride; metabolic disease;
KW   gene therapy; anorectic; immunomodulator; antidiabetic; hypotensive;
KW   cardiant; osteopathic; antilipemic.
XX
OS   Homo sapiens.
XX
XX
PN   WO2003075945-A2.
XX
PD   18-SEP-2003.
XX
PF   14-MAR-2003; 2003WO-EP002714.
XX
PR   14-MAR-2002; 2002EP-00005882.
PR   15-MAR-2002; 2002EP-00006012.
PR   20-MAR-2002; 2002EP-00006271.
PR   25-MAR-2002; 2002EP-00006810.
XX
PA   (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
XX
PI   Eulenberg K, Steuernagel A, Haeder T, Broenner G;
XX
DR   WPI; 2003-748334/70.
DR   N-PSDB; ACH00820.

```
XX
PN  New pharmaceutical composition comprising a nucleic acid molecule
PT  encoding proteins regulating the energy homeostasis and metabolism of
PT  triglycerides useful for detecting or preventing metabolic diseases, e.g.
PT  obesity.
XX
PS  Claim 3; Fig 11C; 140pp; English.
XX
CC
CC  The present invention relates to pharmaceutical compositions comprising
CC  the coding sequences shown in ACH00815-ACH00827, or their encoded
CC  proteins (shown in ABG75054, ABG75056-ABG75067). These are proteins
CC  involved in the metabolism of triglycerides and in energy homeostasis,
CC  and their coding sequences. The composition is useful for the manufacture
CC  of an agent for detecting, verifying, treating, alleviating or preventing
CC  disorders, including metabolic diseases such as obesity and other body-
CC  weight regulation disorders as well as related disorders such as
CC  metabolic syndrome, eating disorder, cachexia, diabetes mellitus,
CC  hypertension, coronary heart disease, hypercholesterolaemia,
CC  dyslipidaemia, osteoarthritis or gallstones, in cell, cell masses,
CC  organs or subjects. The coding sequences can be used in the production of
CC  transgenic animals which under- or over-produce the gene of interest. The
CC  present sequence is a protein of the invention
XX
SQ  Sequence 314 AA;
XX

Alignment Scores:
Pred. No.:
Score:               1603.00         Length:         314
Percent Similarity:  100.0%          Matches:        314
Percent Identity:    100.0%          Conservative:   0
Best Local Similarity: 56.3%         Mismatches:     0
Query Match:         3.97e-128       Indels:         0
DB:                                  Gaps:           0

US-09-888-264-2 (1-1503) x ABG75060 (1-314)

Qy   112 ATGGCGGCGACGGCCGGAGTGCGCGGGGCCCCGGGGGGGATGAGACGGGAGAAGCCCCGGTACCTCCCCT 171
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MetAlaAlaThrAlaSerIleuAlaGlyAlaLeuGlyIleGlyIleuAspGlyLysProArgThrSerPro 20

Qy   172 AAGTCCGGTCAAGTTCCTGTTTGGGGGGCCTGGCCGGGAGGGGAGCGTACAGTTTTTGTCCAG 231
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    21 LysSerValLysPheLeuPheGlyGlyLeuAlaGlyMetGlyAlaThrValPheValGln 40

Qy   232 CCCCTGGACCTGGTGAAGAACCGGATGCAGTTGAGCGGGGAAGGGGCCAAGACTCGGAGAG 291
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Db    41 ProLeuAspLeuValLysAsnArgMetGlnLeuSerGlyGluGlyAlaLysThrArgGlu 60

Qy   292 TACAAAACCAGCTTCCATGCCCTCACCAGTATCCTGAAGGCAGAAGGCCTGAGGGGCATT 351
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TyrLysThrSerProPheHisAlaLeuThrSerIleLeuLysAlaGlyValLeuArgGlyIle 80

Qy   352 TACACTGGGCGTGTCGGCGTCTGGCCCTGCGCTACCACCTACCCGCCCTTGGC 411
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    81 TyrThrGlyLeuSerAlaGlyLeuLeuArgGlnAlaThrThrTyrThrArgLeuGly 100

Qy   412 ATCTATACCGGTGCTGTTTGAGCGGCCTGACTGGGGGTACTCCCCTGGCTTTCTCG 471
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   101 IleTyrThrValLeuPheGluArgProAspGlyThrProProGlyPheLeu 120

Qy   472 CTGAAGGCTGTGATTGGCCATGACCCGCAGGGTGCCACTGGTGCCTTTGGGGACCAGCC 531
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 LeuLysAlaValIleGlyMetThrAlaGlyAlaThrGlyAlaPheGlyAspGlnThrProAla 140

Qy   532 GAAGTGGGTCTTATCCGCATGACTGCCGATGGCTTCCAGCTGACCAGCCCGTGGC 591
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   141 GluValAlaLeuIleArgMetThrAlaAspGlyArgLeuProAlaAspProGlnArgGly 160

Qy   592 TACAAAAATGTGTTTAACCCCCTGCAATTCGAATCCACCCCGGAGAGAGGGGTCTCCACACTG 651
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   161 TyrLysAsnValPheAsnAlaLeuLeuIleArgIleGluThrArgGluGlyValGlyValLeuThrLeu 180

Qy   652 TGGCGGGGGCTGCATCCCTACCATGGCTCGGGCCGTGCTCGTCGTGCCCAGCTCGGC 711
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TrpArgGlyCysIleProThrMetAlaArgAlaValValValAsnAlaAlaGlnLeuAla 200

Qy   712 TCCTTACTCCCAATCCAAGCAGAGTTCTTACTGGACTCAGGCTACTTCCTCGACACATCTTG 771
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   201 SerTyrSerGlnSerLysLysGlnPheLeuLeuAspSerGlyTyrPheSerArgAspAsnIleLeu 220

Db   221 CysHisPheCysAlaSerMetIleSerGlyLeuValThrThrAlaAlaSerMetProVal 240

Qy   832 GACAATTGCCAAGACCCGAATCCAGAACATGCGGATGATTGGAGAAGCCGGGAATACAAG 891
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 AspIleAlaLysThrArgIleGlnAsnMetArgMetIleGlyGluAlaGlyAsnThrLys 260

Qy   892 AACCGGGTCTGGGACCTGGCTGTTCAAAAGTTGTCCGGCTACGAGGGGGCTTCTTCAGCGTCGTGGGAAG 951
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   261 AsnGlyValTrpAspLeuAlaValGlnLysLeuSerGlyTyrGluGlyAlaSerSerAlaSerTrpGlu 280

Qy   952 GGCTTCACGCCGTACTATGCCCGGCTGGGGCCCCACACCGTCTCCACCTTCATCTTCTTG 1011
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   281 GlyPheThrProTyrTyrAlaArgLeuGlyProHisThrValSerThrPheIlePheLeu 300

Qy  1012 GAGCAGGATGAACAAGGGCCTACAACGGTCTCTTCCTCAGGTGGC 1053
         |||||||||||||||||||||||||||||||||||||||||||||
Db   301 GluGlnMetAsnLysAlaTyrTyrLysAlaArgLeuPheLeuSerGly 314

RESULT 2

AD163106
AD163106 standard; protein; 314 AA.

ID  AD163106 standard; protein; 314 AA.
XX
AC  AD163106;
XX
DT  22-APR-2004 (first entry)
XX
DE  Human apoptosis-associated protein SEQ ID 549.
XX
KW  apoptosis; cell death; cytostatic; neuroprotective; immunosuppressive;
KW  antirheumatic; antiarthritic; dermatological; antiinflammatory;
KW  hepatotropic; virucide; nootropic; anticonvulsant; antiparkinsonian;
KW  vasotropic; cerebroprotective; antialcoholic; gene therapy; tumour;
KW  autoimmune disease; degenerative disease; viral infection; leukaemia;
KW  carcinoma; sarcoma; multiple sclerosis; rheumatoid arthritis; diabetes;
KW  lupus; hepatitis; influenza viruses; Alzheimer's disease;
KW  Huntington's disease; Parkinson's diseases; reperfusion injury; stroke;
KW  alcoholic liver disease; human.
OS  Homo sapiens.
PN  WO200305802l-A2.
PD  17-JUL-2003.
PF  13-JAN-2003; 2003WO-EP000270.
PR  11-JAN-2002; 2002DE-01000856.
PA  (XANT-) XANTOS BIOMEDICINE AG.
PI  Koenig-Hoffman K, Kazinski M, Schaefer R, Kasper B;
DR  WPI; 2003-542134/51.
PT  New nucleic acids involved in apoptosis, useful for diagnosis and
PT  treatment of e.g. tumors and degenerative disease, also related proteins,
PT  antibodies and modulators.
PS  Claim 1b; SEQ ID NO 549; 517pp; German.
CC  This invention describes novel nucleic acid molecules that are associated
CC  with apoptosis and encode a polypeptide and are derived from a normalised
CC  gene library (embryonic or liver) or clone collections, and the extent of
CC  apoptosis measured by cell death detection assay or the CPRG assay
CC  (measuring loss of membrane integrity). The products of the invention
```

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Run on: February 1, 2006, 13:33:41 ; Search time 11.0464 Seconds
                                      (without alignments)
                                      2618.292 Million cell updates/sec

OM nucleic - protein search, using frame_plus_n2p model

Title: US-09-888-264-2
Perfect score: 2847
Sequence: 1 cctcgtgcaggcgtgcgcg...........ccaaaaaaaaaaaaaaa 1503

Scoring table: BLOSUM62
               Xgapop 10.0 , Xaapext   0.5
               Ygapop 10.0 , Ygapext   0.5
               Fgapop 6.0 , Fgapext   7.0
               Delop 6.0 , Delext   7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p_model -DEV=xlp
-Q=/abss/ABSSWEB_epool/US09880264/runat_01022006_131840_14810/app_query.fasta_1
-DB=PIR -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abss02p
-USER=US09880264 @CCN 1_1_77 @runat_01022006_131840_14810 -NCPU=6 -ICPU=3
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -LONGLOG=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_80:*
       1: pir1:*
       2: pir2:*
       3: pir3:*
       4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1600	56.2	314	2	A56650	2-oxoglutarate car
2	1545	54.3	314	2	A36305	2-oxoglutarate/mal
3	1058.5	37.2	323	2	T25459	hypothetical prote
4	602.5	21.2	302	2	S65040	2-oxoglutarate/mal
5	598	21.0	302	2	S65042	2-oxoglutarate/mal
6	584.5	20.5	297	2	T07405	oxoglutarate/malat
7	583	20.5	313	2	D4613	hypothetical prote
8	554	19.5	313	2	T05577	uncoupling protein
9	527.5	18.5	331	2	T51899	probable 2-oxoglut
10	510	17.9	290	2	S44091	oxoglutarate/malat
11	498	17.5	325	2	JC7553	brain mitochondria
12	468	16.4	305	2	H86274	F7A19.22 protein -
13	459.5	16.1	298	2	S51351	hypothetical prote
14	445.5	15.6	282	2	T49628	probable dicarboxy
15	438.5	15.4	307	2	G01858	uncoupling protein
16	434.5	15.3	306	2	T07793	uncoupling protein
17	426	15.0	312	2	JC5522	uncoupling protein
18	422.5	14.8	307	2	A26294	uncoupling protein
19	415.5	14.6	306	2	A31106	mitochondrial unco
20	415	14.6	307	2	S34268	uncoupling protein
21	413	14.5	320	2	T37603	probable oxaloacet
22	411.5	14.5	306	2	T47570	uncoupling protein
23	402.5	14.1	306	2	T52024	uncoupling protein
24	400	14.0	306	2	A32446	uncoupling protein
25	365	12.8	288	2	S03603	mitochondrial uO
26	357.5	12.6	324	2	S25357	hypothetical unco
27	331	11.6	343	2	S15253	hypothetical prote
28	302	10.6	322	2	S57116	probable carrier p
29	280.5	9.9	307	2	S60949	probable phosphate
30	270.5	9.5	309	2	T48156	hypothetical prote
31	264.5	9.3	392	2	T16533	hypothetical prote
32	257	9.0	310	2	T05350	adenylate transloc
33	256.5	9.0	352	2	S69050	probable membrane
34	247	8.7	310	2	T01729	mitochondrial solu
35	238	8.4	436	2	JQ1459	Bt1 protein precur
36	233.5	8.2	331	2	F84823	probable peroxisom
37	232	8.1	475	2	T50686	probable peroxisom
38	231.5	8.1	358	2	T09109	peroxisomal Ca-dep
39	231.5	8.1	377	2	S36081	envelope protein L
40	228	8.0	299	2	S44554	probable carrier P
41	224.5	7.9	335	2	S50453	citrate transport
42	223.5	7.9	415	2	S50451	hypothetical prote
43	223	7.8	902	2	T48171	hypothetical prote
44	221	7.8	291	2	S54495	probable carrier P
45	220.5	7.7	311	2	G01789	citrate transporte

ALIGNMENTS

RESULT 1
A56650
2-oxoglutarate carrier protein - human
C;Species: Homo sapiens (man)
C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: A56650; S29598
R;Iacobazzi, V.; Palmieri, F.; Runswick, M.J.; Walker, J.E.
DNA Seq. 3, 79-88, 1992
A;Title: Sequences of the human and bovine genes for the mitochondrial 2-oxoglutarate ca
A;Reference number: A56650; MUID:93091249; PMID:1457818
A;Accession: A56650
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-314 <IAC>
A;Cross-references: UNIPROT:Q02978; UNIPARC:UPI000016A206; EMBL:X66114; NID:g23843; PIDN
C;Accession: A56650; S29598
C;Genetics:
A;Introns: 32/2; 83/2; 152/2; 182/3; 246/2; 263/3
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: duplication; mitochondrion; transmembrane protein
C;Note: sequence extracted from NCBI backbone
F;18-109/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;116-209/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;216-307/Domain: ADP,ATP carrier protein repeat homology <ACP3>

US-09-888-264-2 (1-1503) x A56650 (1-314)

Alignment Scores:
Pred. No.:   4.44e-105
Score: 1600.00
Percent Similarity: 100.0%
Best Local Similarity: 99.7%
Query Match: 56.2%
DB: 2

Length:	314			
Matches:	313			
Conservative:	1			
Mismatches:	0			
Indels:	0			
Gaps:	0			

Qy   112 ATGGCGGGGACGGCGAGTGCCGGGGGGGCCCGGCGGGGGGGGGGGGGATAGGACGGGGAAGCCCCCGTATACCTCCCCT 171
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Db   1 MetAlaAlaThrAlaSerAlaGlyAlaGlyGlyMetAspGlyLysProArgThrSerPro 20

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Qy    172  AAGTCCGTCAAGTTCCTGTTTGGGGGCCCTGGCCCGGGAGGAGCTACAGTTTTTGTCCAG  231
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Db     21  LysSerValLysPheLeuPheGlyGlyLeuAlaGlyMetGlyAlaThrValPheValGln  40

Qy    232  CCCCTGGACCTGGTGAAGAACCCGGATGCAGTTGAGCGCGGGGAAGGGGCCAAGACTCGAG  291
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     41  ProLeuAspLeuValLysAsnProAspAlaValGluArgGlyGluGlyAlaLysThrArgGlu  60

Qy    292  TACAAAAACCAGCTTCCATGCCCTCACCAGTATCCTGAAGGCAGAAGGCCTGAGGGGCATT  351
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  TyrLysThrSerPheHisAlaLeuThrSerIleLeuGlyGlnGluGlyLeuArgGlyIle  80

Qy    352  TACACTGGGGCTGTGCGGCCTGCCTGGCTCCGTGCGGTCAGCGGCCACCTACACTACCCGGCTTGGC  411
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     81  TyrThrGlyLeuSerAlaGlyLeuLeuArgGlnAlaThrTyrThrThrThrArgLeuGly  100

Qy    412  ATCTATACCGTGCTGTTTGAGCCGCTGACTGGGGCGTGATGGTACTCCCCTGGCTTTCTG  471
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    101  IleTyrThrValLeuPheGluArgLeuThrGlyAlaAspGlyThrProGlyPheLeu  120

Qy    472  CTGGAAGGCTGTGTGATTGGCATGACCGCAGGTGTGCCACTCGGTGTGCTTTGTGGGGAACACCAGCC  531
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  LeuLysAlaLValIleGlyMetThrAlaGlyValProLeuGlyValLeuCysGlyAsnThrSer  140

Qy    532  GAAGTGGGTCTTATACCGGCATGACCGCCATGGGCCCGGCTTCCAGCTGACCAGCCGCGTGGC  591
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141  GluValGlyLeuIleArgMetThrAlaAlaSpGlyArgLeuProAlaAspProGlnArgGlyGly  160

Qy    592  TACAAAAATGTGTTTAACGGCCCGGTTGGAATCAACCCGGGGAGAGAGGGTGTCTTCCACACTG  651
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161  TyrLysAsnValPheAsnGlyProValGlyIleAsnProGlyGluGlyGlyValPheLeuHisThrVal  180

Qy    652  TGGCGGCGGCTGCATCCCTTACCATGGCCTCGGGCGTCGTTGCCCAGCTCGCC  711
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  TrpArgGlyCysIleProThrMetAlaArgGlaLaValValVaLAsnAlaLaAlaGlnLeuAla  200

Qy    712  TCCTACTCCCAATCCAAGCAGTTCTTACTGGACTCAGCGTACTTCTCTGACAACATCTTG  771
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    201  SerTyrSerGlnSerLysGlnPheLeuLeuAspSerGlyTyrPheSerAspAsnIleLeu  220

Qy    772  TGCCACTTCTGTGCCAGCATGATCAGCGGCGTCGTTGTCACCACTGCTGCTCCATGCCTGTG  831
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    221  CysHisPheCysAlaSerMetIleSerGlyValVaLValValThrThrAlaAlaSerMetProVal  240

Qy    832  GACATTGCCAAGACACCCGAAATCCAGGAACATGCCGGATGATTGATGGGGAAGCCGGAATACAG  891
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  AspIleAlaLysThrArgGluIleGlnAsnMetProAspGluGlyLysProGluTyrLys  260

Qy    892  AACGGGCGTGGACCTGCTGTTCAAAGTTTCCGTACGAGGGGGCTTCTTCAGCCTGTGGAAG  951
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    261  AsnGlyLeuAspValLeuPheLysValArgTyrGluGlyPhePheSerLeuTrpLys  280

Qy    952  GGGCTTCACGGCGGTACTATGCCCCCACCACGGTCCTCACCTTCAATCTTCTTG  1011
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    281  GlyPheThrProTyrTyrAlaArgLeuGlyProHisThrValLeuThrPheIlePheLeu  300

Qy   1012  GAGCAGATGAACAAGGCCTACAAGCGTCTTCCTCCAGTGGC  1053
           |||||||||||||||||||||||||||||||||||||||||
Db    301  GluGlnMetAsnLysAlaTyrLysArgLeuPheLeuSerGly  314
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A;Residues: 1-314 <RUN>
A;Cross-references: UNIPROT:P22292; UNIPARC:UPI000016753C; GB:M06662; GB:J05296; NID:g16?
R;Iacobazzi, V.; Palmieri, F.; Runswick, M.J.; Walker, J.E.
A;Title: Sequences of the human and bovine genes for the mitochondrial 2-oxoglutarate ca
A;Reference number: A56650; MUID:93091249; PMID:1457818
DNA Seq. 3, 79-88, 1992

A;Accession: B56650
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-314 <IA2>
A;Cross-references: UNIPARC:UPI000016753C; EMBL:X66115; NID:g931; PIDN:CAA46906.1; PID:g3?
A;Note: sequence extracted from NCBI backbone (NCBIN:120086, NCBIP:120087)
R;Bisaccia, F.; Zara, V.; Capobianco, L.; Iacobazzi, V.; Mazzeo, M.; Palmieri, F.
Biochim. Biophys. Acta 1292, 281-288, 1996

A;Title: The formation of a disulfide cross-link between the two subunits demonstrates th
A;Accession: S65731
A;Status: preliminary
A;Molecule type: protein
A;Residues: 148-160 <BIS>
A;Cross-references: UNIPARC:UPI00001177A24
R;Bisaccia, F.; Capobianco, L.; Brandolin, G.; Palmieri, F.
Biochemistry 33, 3705-3713, 1994

A;Title: Transmembrane topography of the mitochondrial oxoglutarate carrier assessed by r
A;Reference number: A54249; MUID:94190892; PMID:8142370
A;Accession: A54249
A;Status: preliminary
A;Molecule type: protein
A;Residues: 6-15,23-32,40-49,62-71,104-113,170-179,183-192 <BI2>
A;Cross-references: UNIPARC:UPI00001177A25; UNIPARC:UPI00001177A26; UNIPARC:UPI00001177A27;
R;Bisaccia, F.; Capobianco, L.; Mazzeo, M.; Palmieri, F.
FEBS Lett. 392, 54-58, 1996

A;Title: The mitochondrial oxoglutarate carrier protein contains a disulfide bridge betwe
A;Reference number: S71377; MUID:96354876; PMID:8769314
A;Accession: S71377
A;Status: preliminary
A;Molecule type: protein
A;Residues: 148-160;189-200 <BIW>
A;Cross-references: UNIPARC:UPI00001177A24; UNIPARC:UPI00001177A2C
A;Experimental source: heart
C;Genetics:
C;Introns: 32/2; 83/2; 246/2; 263/3
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: duplication; mitochondrion; transmembrane protein
F;18-109/Domain: ADP,ATP carrier protein homology <BI2>
F;116-209/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;216-307/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;221-224/Disulfide bonds: #status experimental

RESULT 2
A36305

2-oxoglutarate/malate carrier protein, inner mitochondrial membrane - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Mar-1991 #sequence revision 28-Mar-1991 #text change 09-Jul-2004
C;Accession: A36305; B56650; S65731; A54249; S71377; S29597
R;Runswick, M.J.; Walker, J.E.; Bisaccia, F.; Iacobazzi, V.; Palmieri, F.
Biochemistry 29, 11033-11040, 1990
A;Title: Sequence of the bovine 2-oxoglutarate/malate carrier protein: structural relati
A;Reference number: A36305; MUID:91105033; PMID:2271695
A;Accession: A36305
A;Status: preliminary
A;Molecule type: mRNA

US-09-888-264-2 (1-1503) x A36305 (1-314)

Alignment Scores:
Pred. No.:
Score: 3.38e-101   Length: 314
                   1545.00   Matches: 302
Percent Similarity:
Percent Identity: 97.1%   Conservative: 3
                    96.2%   Mismatches: 9
Best Local Similarity: Indels: 0
Query Match: 54.3%   Gaps: 0
DB: 2

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           ||:|||||||||:|||||||||||||||||||||||||||||||:|||||||||||||||||
Db      1  MetAlaAlaAlaThrAlaSerProGlyAlaSerGlyMetAspGlyArgLysProArgThrSerPro  20

Qy    172  AAGTCCGTCAAGTTCCTGTTTGGGGGCCCTGGCCCGGGAGGAGCTACAGTTTTTGTCCAG  231
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     21  LysSerValLysPheLeuPheGlyGlyLeuAlaGlyMetGlyAlaThrValPheValGln  40

Qy    232  CCCCTGGACCTGGTGAAGAACCCGGATGCAGTTGAGCGCGGGGAAGGGGCCAAGACTCGAG  291
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Db     41  ProLeuAspLeuValLysAsnProAspAlaValGluArgGlyGluGlyAlaLysThrArgGlu  60

Qy    292  TACAAAAACCAGCTTCCATGCCCTCACCAGTATCCTGAAGGCAGAAGGCCTGAGGGGCATT  351
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  TyrLysThrSerPheHisAlaLeuThrSerIleLeuGlyGlnGluGlyLeuArgGlyIle  80
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OM nucleic - protein search, using frame_plus_n2p

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on: February 1, 2006, 13:19:06 ; Search time 71.6014 Seconds
(without alignments)
2961.978 Million cell updates/sec

Title: US-09-888-264-2
Perfect score: 2847
Sequence: 1 cctcgtgcaggcgtcgcg..........ccaaaaaaaaaaaaaaa 1503

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 4332886

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US09888264 @CGN 1 1 580 @runat_01022006_131838_14779 -NCPU=6 -ICPU=3
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1603	56.3	314	2	Q6IBH0_HUMAN	Q6ibh0 homo sapien
2	1598	56.1	313	2	M2OM_HUMAN	Q02978 homo sapien
3	1596	56.1	314	2	Q5RFJ5_PONPY	Q5rfj5 pongo pygma
4	1554	54.6	314	2	Q5SX53_MOUSE	Q5sx53 mus musculu
5	1549	54.4	313	2	M2OM_MOUSE	Q9cr62 mus musculu
6	1545	54.3	314	2	Q5E9W4_BOVIN	Q5e9w4 bos taurus
7	1540	54.1	313	2	M2OM_BOVIN	P22292 bos taurus
8	1531	53.8	313	1	M2OM_RAT	P97700 rattus norv
9	1418	49.8	305	2	Q56FL1_XENLA	Q56fl1 xenopus lae
10	1407	49.4	305	2	Q6INH3_XENTR	Q6inh3 xenopus tro
11	1382	48.5	308	2	Q6IQ89_BRARE	Q6iq89 brachydanio
12	1363	47.9	313	2	Q4TA26_TETNG	Q4ta26 tetraodon n
13	1258	44.2	252	2	Q9CTC7_MOUSE	Q9ctc7 mus musculu
14	1060	37.2	307	2	Q61QH3_CAEBR	Q61qh3 caenorhabdi
15	1053.5	37.0	306	2	P90992_CAEEL	P90992 caenorhabdi
16	957	33.6	193	2	Q5SX46_MOUSE	Q5sx46 mus musculu
17	919.5	32.3	317	2	Q9VAJ9_DROME	Q9vaj9 drosophila
18	891.5	31.3	292	2	Q5TN06_ANOGA	Q5tn06 anopheles g
19	840.5	29.5	311	2	Q9VZ93_DROME	Q9vz93 drosophila
20	839.5	29.5	311	2	Q8SX84_DROME	Q8sx84 drosophila
21	781	27.4	301	2	Q9VZ94_DROME	Q9vz94 drosophila
22	716	25.1	318	2	Q54PY7_DICDI	Q54py7 dictyosteli
23	606	21.3	307	2	Q66PW8_SACOF	Q66pw8 saccharum o
24	606	21.3	309	2	Q53PA7_ORYSA	Q53pa7 oryza sativ
25	602.5	21.2	302	2	Q42422_PANMI	Q42422 panicum mil
26	598	21.0	302	2	Q40918_PANMI	Q40918 panicum mil
27	596	20.9	299	2	Q6T871_9ROSI	Q6t871_9rosi citrus juno
28	596	20.9	313	2	Q59IV3_MESCR	Q59iv3 mesembryant
29	591	20.8	321	2	Q6YX13_ORYSA	Q6yx13 oryza sativ
30	590	20.7	298	2	Q8SM0_ARATH	Q9c5m0 arabidopsis
31	589	20.7	300	2	Q8SF02_TOBAC	Q8sf02 nicotiana t
32	585	20.5	325	2	Q66PX3_SACOF	Q66px3 saccharum o
33	585	20.5	297	2	Q8SF03_TOBAC	Q8sf03 nicotiana t
34	585	20.5	297	2	Q9FSF4_TOBAC	Q9fsf4 nicotiana t
35	585	20.5	297	2	Q8SF04_TOBAC	Q8sf04 nicotiana t
36	585	20.5	306	2	Q60EY2_ORYSA	Q60ey2 oryza sativ
37	584.5	20.5	297	2	Q60EY9_ORYSA	Q60ey9 oryza sativ
38	583	20.5	313	2	Q43649_SOLTU	Q43649 solanum tub
39	581	20.4	331	2	Q9SJY5_ARATH	Q9sjy5 arabidopsis
40	579	20.3	313	2	Q66PX4_SACOF	Q66px4 saccharum o
41	574	20.2	313	2	Q8LDF6_ARATH	Q8ldf6 arabidopsis
42	571.5	20.1	313	2	Q94K32_ARATH	Q94k32 arabidopsis
43	565.5	19.9	319	2	Q7RMU4_PLAYO	Q7rmu4 plasmodium
44	561.5	19.7	319	2	Q4XPT4_PLACH	Q4xpt4 plasmodium
45	556	19.5	285	2	Q7QBN6_ANOGA	Q7qbn6 anopheles g

ALIGNMENTS

RESULT 1
Q6IBH0_HUMAN
ID   Q6IBH0_HUMAN PRELIMINARY;   PRT;   314 AA.
AC   Q6IBH0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   SLC25A11 protein.
GN   Name=SLC25A11;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CR456834; CAG33115.1; -; mRNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR   GO; GO:0005488; F:binding; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
KW   Transmembrane; Transport.
SQ   SEQUENCE   314 AA;   34061 MW;   9D61F817089FF5AA CRC64;

Alignment Scores:
Pred. No.:   3.6e-97
Score: 1603.00   Length: 314
Percent Similarity: 100.0%   Matches: 314
                              100.0%   Conservative: 0
                                          Mismatches: 0
Best Local Similarity: 100.0%   Indels: 0
Query Match: 56.3%   Gaps: 0

DB: 2

US-09-888-264-2 (1-1503) x Q6IBH0_HUMAN (1-314)

Qy   112 ATGGCGGCGACGGCGACGGCCGGGAGCCCCGGGGGATAGACGGGAAGCCCCGTACTTCCCT 171
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MetAlaAlaThrAlaSerAlaGlyAlaGlyGlyIleAspGlyLysProArgThrSerPro 20

```
Qy  172  AAGTCCGTCAAGTTCCTTGTTTGGGGGCCTTGGCCGGGGAGGTACAGTTTTTGTCCAG  231
              LysSerValLysPheLeuPheLeuGlyGlyLeuAlaGlyMetGlyValAlaThrValPheValGln
Db   21  ...  40

Qy  232  CCCCTGGACCTGGTTGAAGAAACCGGATGCAGTTGAGGGGGGAGGACTCGAGAG  291
              ProLeuAspLeuValGluAsnArgMetGlnLeuSerGlyGluGlyValAlaLysThrArgGlu
Db   41  ...  60

Qy  292  TACAAAAACCAGCTTCCATGCCCTACCCAGTATCCTGAAGGACAGAAGGGGCATT  351
              TyrLysThrSerPheHisAlaLeuThrSerIleLeuLysAlaGluGlyLeuArgGlyIle
Db   61  ...  80

Qy  352  TACACTGGGCTGTCGGGCTGGGCTGGCCTTACCACTACACCACTACCCGGCTTGGC  411
              TyrThrGlyLeuSerAlaGlyLeuLeuArgGlnAlaThrTyrThrThrThrArgLeuGly
Db   81  ...  100

Qy  412  ATCTATACCGTGCTGTTTGTTTGAGCGGCCTGACTGGGCTGGGGTTACTCCCCCTGGCTTTCTG  471
              IleTyrThrValLeuPheGluArgLeuThrGlyAlaAspGlyThrProProGlyPheLeu
Db  101  ...  120

Qy  472  CTGAAAGGCTGTGATTGGGGATGACCGCACGTGCCACTGTTGTGGGGAACACCAGCC  531
              LeuLysAlaValIleGlyMetThrAlaGlyValAlaThrGlyAlaValThrGlnProAla
Db  121  ...  140

Qy  532  GAAGTGGCTGTCTTATCCGGATGACTGGCCCGGCTTCCAGCTGGACCCGGCTGGC  591
              GluValLeuLysIleArgMetThrAlaAspGlyArgLeuProAlaAspIleArgArgGly
Db  141  ...  160

Qy  592  TACAAAAATGTGTTTAACGCCCTGATTCGAATCACCCGGGAAGAGGGTGTCTTCCACACTG  651
              TyrLysAsnValPheAsnAlaLeuIleArgIleThrArgGluGluGlyValLeuThrLeu
Db  161  ...  180

Qy  652  TGGCGGGGCTGCATCCCTACCATGGCTCGGGCGGCTGTCGTGAATGCTGCCCAGCTCGCC  711
              TrpArgGlyCysIleProThrMetAlaArgAlaValValValAsnAlaAlaGlnLeuAla
Db  181  ...  200

Qy  712  TCCTACTCCCAATCCAAGCAGTTCTTACTGGACTCTGGCTACTTCTCTGACAACATCTTG  771
              SerTyrSerGlnSerLysGlnPheLeuLeuAspSerGlyTyrPheSerAspAsnIleLeu
Db  201  ...  220

Qy  772  TGCCACTTCTGTGCCAGCATGATCAGCGGGCTCGTTGTCACCACTGCTGCCTCCATGCCTGTG  831
              CysHisPheCysAlaSerMetIleSerGlyLeuValThrThrAlaAlaSerMetProVal
Db  221  ...  240

Qy  832  GACATTGCCAAGACCCGAATCCAGAACATGCGGATGATTGATGGGAAGCCCGGAATACAAG  891
              AspIleAlaLysThrArgIleGlnAsnMetArgMetIleAspGlyLysProGluTyrLys
Db  241  ...  260

Qy  892  AACGGGCTGGACGTGCTGTTCAAAGTTGCTCGCTACGAGGGCTTCTTCAGCCTGTGGAAG  951
              AsnGlyLeuAspValLeuPheLysValAlaArgTyrGluGlyPhePheSerLeuTrpLys
Db  261  ...  280

Qy  952  GGCTTCACGCCGTACTATGCCCGGCTGGGCCCCACACGGTCCTCACCTTCATCTTCTG  1011
              GlyPheThrProTyrTyrAlaArgLeuGlyProHisThrValLeuThrPhePheLeuPheLeu
Db  281  ...  300

Qy 1012  GAGCAGATGAACAAAGGCCTACAAGGCGTCTTCTTCAGTGGC  1053
              GluGlnMetAsnLysAlaTyrTyrLysAlaArgLeuGluPheLeuSerGly  314
Db  301  ...  300
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RESULT 2
M2OM_HUMAN

ID   M2OM_HUMAN   STANDARD;   PRT;   313 AA.
AC   Q02978; O75537; O96P7;
DT   01-JUN-1993 (Rel. 26, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Mitochondrial 2-oxoglutarate/malate carrier protein (OGCP) (Solute
DE   carrier family 25 member 11).
GN   Name=SLC25A11; Synonyms=SLC20A4;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=93091249; PubMed=1457818;
RA   Iacobazzi V., Palmieri F., Runswick M.J., Walker J.E.;
RT   "Sequences of the human and bovine genes for the mitochondrial 2-
RT   oxoglutarate carrier.";
RL   DNA Seq. 3:79-88(1992).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Brain;
RA   Yu W., Gibbs R.A.;
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Muscle, and Uterus;
RX   MEDLINE=22382257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   PROTEIN SEQUENCE OF 1-16, CLEAVAGE OF INITIATOR METHIONINE,
RP   ACETYLATION SITE ALA-1, AND MASS SPECTROMETRY.
RC   TISSUE=B-cell lymphoma;
RA   Bienvenut W.V.;
RL   Unpublished observations (JUN-2005).
CC   -!- FUNCTION: Catalyzes the transport of 2-oxoglutarate across the
CC   inner mitochondrial membrane in an electroneutral exchange for
CC   malate or other dicarboxylic acids, and plays an important role in
CC   several metabolic processes, including the malate-aspartate
CC   shuttle, the oxoglutarate/isocitrate shuttle, in gluconeogenesis
CC   from lactate, and in nitrogen metabolism.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC   inner membrane.
CC   -!- SIMILARITY: Belongs to the mitochondrial carrier family.
CC   -!- SIMILARITY: Contains 3 Solcar repeats.
DR   EMBL; X66114; CAA46905.1; -; Genomic_DNA.
DR   EMBL; AF070548; AAC28637.1; -; mRNA.
DR   EMBL; BC006508; AAH06508.1; -; mRNA.
DR   EMBL; BC006519; AAH06519.1; -; mRNA.
DR   EMBL; BC016294; AAH16294.1; -; mRNA.
DR   EMBL; BC017170; AAH17170.1; -; mRNA.
DR   PIR; A56650; A56650.
DR   Ensembl; ENSG00000108528; Homo sapiens.
DR   HGNC; HGNC:10981; SLC25A11.
DR   H-InvDB; HIX0013454; -.
DR   MIM; 604165; -.

OM nucleic - protein search, using frame_plus_n2p model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run On: February 1, 2006, 13:54:36 ; Search time 10.0162 Seconds
                 (without alignments)
                 2481.215 Million cell updates/sec

Title: US-09-888-264-2
Perfect score: 2847
Sequence: 1 cctcgtgccaggcgtgcgcg..........ccaaaaaaaaaaaaaaa 1503

Scoring table: BLOSUM62
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                 Xgapop 10.0 , Xgapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 572060 seqs, 82675679 residues
                 Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Total number of hits satisfying chosen parameters: 1144120

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=gto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Issued_Patents_AA:*
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                 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
                 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Pred. No.	Query Match	Length	DB	ID	Description
1	586	20.6	299	2		US-09-463-239-35	Sequence 35, Appl
2	513	18.0	313	2		US-09-248-796A-17621	Sequence 17621, A
3	509.5	17.9	355	2		US-09-463-239-30	Sequence 30, Appl
4	500	17.6	322	2		US-09-949-016-8722	Sequence 8722, Ap
5	500	17.6	322	2		US-09-949-016-8723	Sequence 8723, Ap
6	495	17.4	335	2		US-09-482-273-118	Sequence 118, App
7	468.5	16.5	290	2		US-09-743-847-2	Sequence 2, Appli
8	468.5	16.5	300	2		US-09-463-239-34	Sequence 34, Appl
9	450	15.8	432	1		US-08-937-466-4	Sequence 4, Appli
10	450	15.8	432	2		US-09-172-528-4	Sequence 4, Appli
11	450	15.8	432	1		US-09-318-199-4	Sequence 4, Appli
12	450	15.8	432	2		US-09-503-579-4	Sequence 4, Appli
13	440	15.5	308	1		US-08-937-466-2	Sequence 2, Appli
14	440	15.5	308	2		US-09-172-528-2	Sequence 2, Appli
15	440	15.5	308	1		US-09-318-199-2	Sequence 2, Appli
16	440	15.5	308	2		US-09-503-579-2	Sequence 2, Appli
17	438.5	15.4	307	2		US-09-743-847-3	Sequence 3, Appli
18	438.5	15.4	307	2		US-10-037-417-87	Sequence 87, Appl
19	438.5	15.4	309	2		US-09-949-016-10401	Sequence 10401, A
20	434.5	15.3	306	2		US-10-009-962-5	Sequence 5, Appli
21	434.5	15.3	306	2		US-09-501-558-5	Sequence 5, Appli
22	433.5	15.2	291	2		US-10-671-628-5	Sequence 5, Appli
23	430.5	15.1	307	2		US-10-037-417-88	Sequence 88, Appl
24	430.5	15.1	307	2		US-10-009-962-7	Sequence 7, Appli
25	428.5	15.1	307	2		US-09-142-565-2	Sequence 2, Appli
26	426	15.0	312	2		US-09-808-457-2	Sequence 2, Appli
27	426	15.0	312	2		US-09-423-410-4	Sequence 4, Appli
28	426	15.0	312	2		US-10-671-628-9	Sequence 9, Appli
29	426	14.9	312	2		US-10-009-962-9	Sequence 9, Appli
30	424	14.9	310	2		US-09-743-847-5	Sequence 5, Appli
31	418	14.7	310	2		US-08-807-861A-56	Sequence 56, Appl
32	415.5	14.6	307	1		US-09-210-681-56	Sequence 56, Appl
33	415.5	14.6	307	2		US-08-946-719A-56	Sequence 56, Appl
34	415.5	14.6	307	2		US-09-547-983-56	Sequence 56, Appl
35	415.5	14.6	307	2		US-10-037-417-91	Sequence 91, Appl
36	415.5	14.6	307	2		US-09-743-847-4	Sequence 4, Appli
37	411.5	14.5	309	2		US-10-001-051B-2	Sequence 2, Appli
38	411.5	14.5	308	2		US-10-671-628-8	Sequence 8, Appli
39	411.5	14.5	309	2		US-09-949-016-9410	Sequence 9410, Ap
40	411.5	14.5	337	2		US-08-518-878B-56	Sequence 56, Appl
41	410.5	14.4	299	2		US-08-470-868A-56	Sequence 56, Appl
42	410.5	14.4	299	1		US-09-210-681-56	Sequence 56, Appl
43	410.5	14.4	309	1		US-08-518-878B-51	Sequence 51, Appl
44	410.5	14.4	309	1		US-08-807-861A-51	Sequence 51, Appl
45	410.5	14.4	309	1		US-08-470-868A-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1
US-09-463-239-35
; Sequence 35, Application US/09463239
; Patent No.: 6700039
; GENERAL INFORMATION:
; APPLICANT: Jepson, Ian
; APPLICANT: Ebneth, Marcus
; APPLICANT: Sonnewald, Uwe
; TITLE OF INVENTION: Genetic Method for Controlling Sprouting
; FILE REFERENCE: 109846.178
; CURRENT APPLICATION NUMBER: US/09/463,239
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/GB98/02023
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: EP 97113118.0
; PRIOR FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Panicum millaceum
US-09-463-239-35

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Pred. No.:   1.56e-42
Score: 586.00
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Query Match: 20.6%

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; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17621
; TYPE: PRT
; LENGTH: 313
; ORGANISM: Candida albicans
US-09-248-796A-17621

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Query Match: 18.0%   Indels: 18
DB: 2   Gaps: 4

US-09-888-264-2 (1-1503) x US-09-248-796A-17621 (1-313)

RESULT 2
US-09-248-796A-17621
Sequence 17621, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: February 1, 2006, 14:41:42 ; Search time 45.3876 Seconds
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Title:
Perfect score: 2847
Sequence: 1 cctcgtgcaggcgtcgcgcg..............ccaaaaaaaaaaaaaaaaa 1503

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                 Fgapop 6.0 , Fgapext 7.0
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Searched: US-09-888-264-2

Total number of hits satisfying chosen parameters: 3735138

Searched: 1867569 seqs, 417829326 residues
                 Listing first 45 summaries

Post-processing: Minimum Match 0%
Maximum DB seq length: 200000000   Maximum Match 100%
Minimum DB seq length: 0

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1603	56.3	314	4	US-10-408-765A-2204	Sequence 2204, Ap
2	1603	56.3	314	5	US-11-408-765A-3015	Sequence 3015, Ap
3	1603	56.3	314	5	US-10-507-617-13	Sequence 13, Appl
4	1603	56.3	314	4	US-10-745-237-370	Sequence 370, App
5	1600	56.2	314	4	US-10-408-765A-498	Sequence 498, Appl
6	1554	54.6	314	5	US-10-507-617-57	Sequence 57, Appl
7	1517	53.3	297	5	US-10-507-617-57	Sequence 56, Appl
8	1060	37.2	310	4	US-10-425-115-211662	Sequence 211662,
9	1060	37.2	312	4	US-10-425-114-59754	Sequence 59754, A
10	1058.5	37.2	323	4	US-10-369-499-5321	Sequence 5321, Ap
11	936	32.9	344	5	US-10-732-923-19208	Sequence 19208, A
12	919.5	32.3	317	5	US-10-732-923-19321	Sequence 19321, A
13	919.5	32.3	317	5	US-11-097-143-816	Sequence 816, App
14	840.5	29.5	311	5	US-10-732-923-19320	Sequence 19320, A
15	840.5	29.5	311	5	US-10-507-617-58	Sequence 58, Appl
16	840.5	29.5	311	6	US-11-097-143-27690	Sequence 27690, A
17	839.5	29.5	294	5	US-10-507-617-55	Sequence 55, Appl
18	839.5	29.5	311	5	US-10-732-923-19319	Sequence 19319, A
19	781	27.4	311	5	US-10-732-923-19326	Sequence 19326, A
20	781	27.4	301	5	US-10-745-237-168	Sequence 168, App
21	781	27.4	301	6	US-11-097-143-555	Sequence 555, App
22	608	21.4	301	4	US-10-437-963-154439	Sequence 154439,
23	607	21.3	309	4	US-10-767-701-45989	Sequence 45989, A
24	603.5	21.2	344	4	US-10-425-114-47724	Sequence 47724, A
25	602.5	21.2	349	4	US-10-732-923-19256	Sequence 19256, A
26	602.5	21.2	301	4	US-10-425-114-47829	Sequence 47829, A
27	599	21.0	301	4	US-10-424-599-220995	Sequence 220995,
28	598	21.0	301	4	US-10-732-923-19255	Sequence 19255, A
29	596	20.9	301	4	US-10-424-599-220998	Sequence 220998,
30	592.5	20.8	305	4	US-10-425-114-63040	Sequence 63040, A
31	592.5	20.8	302	4	US-10-425-115-264201	Sequence 264201,
32	592	20.8	302	4	US-10-425-115-215452	Sequence 215452,
33	590	20.7	300	5	US-10-732-923-19241	Sequence 19241, A
34	590	20.7	300	4	US-10-424-599-276095	Sequence 276095,
35	589	20.7	341	4	US-10-425-114-52234	Sequence 52234, A
36	586	20.6	317	4	US-10-424-599-276094	Sequence 276094,
37	585.5	20.6	285	4	US-10-425-114-41594	Sequence 41594, A
38	585	20.5	295	4	US-10-732-923-19244	Sequence 19244, A
39	585	20.5	297	5	US-10-732-923-19242	Sequence 19242, A
40	585	20.5	297	4	US-10-732-923-19243	Sequence 19243, A
41	585	20.5	327	4	US-10-437-963-125993	Sequence 125993,
42	584.5	20.5	300	5	US-10-732-923-19247	Sequence 19247, A
43	580.5	20.4	300	5	US-10-424-599-217619	Sequence 217619,
44	541.5	19.0	1796	5	US-10-732-923-19283	Sequence 19283, A
45	529	18.6	290	4	US-10-425-115-302750	Sequence 302750,

ALIGNMENTS

RESULT 1
US-10-408-765A-2204

; Sequence 2204, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2204
;   LENGTH: 314
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-408-765A-2204

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Pred. No.:
Score: 5.64e-109
Percent Similarity: 100.0%   1603.00
Best Local Similarity: 56.3%
Query Match: 4

DB:

US-09-888-264-2 (1-1503) x US-10-408-765A-2204 (1-314)

Length: 314
Matches: 314
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

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; APPLICANT:  Taylor, Steven W.
; APPLICANT:  Glenn, Gary M.
; APPLICANT:  Warnock, Dale E.
; TITLE OF INVENTION:  TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION:  IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE:  660088.465
; CURRENT APPLICATION NUMBER:  US/10/408,765A
; CURRENT FILING DATE:  2003-04-04
; NUMBER OF SEQ ID NOS:  3077
; SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 3015
;  TYPE:  PRT
;  LENGTH:  314
;  ORGANISM:  Homo sapiens
US-10-408-765A-3015

Alignment Scores:
Pred. No.:
Score:                       5.64e-109    Length:          314
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Best Local Similarity:       100.0%       Indels:          0
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Db    1 MetAlaAlaThrAlaSerAlaGlyAlaGlyGlyIleAspGlyLysProArgThrSerPro        20

Qy  172 AAGTCCGTCAAGTTCCTTGTTTGGGGCGCTTGGGCGCCGGATGGGAGCTACAGTTTTTTGTCAG   231
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Db   21 LysSerValLysPheLeuPheGlyGlyLeuAlaGlyMetGlyAlaThrValPheValGln        40

Qy  232 CCCCTGGACCTGGTGAAGAACCCGGATGCAGTTGAGGGGGGAAGGGGCCAAGACTCGAGAG     291
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Db   41 ProLeuAspLeuValLysAsnArgMetGlnLeuSerGlyGlyArgGlyAlaLysThrArgGlu    60

Qy  292 TACAAAAACCAGCTTCCATGCCCTACCAGTATCCTGAAGGCAGAAGGCCTGAGGGGCATT     351
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Db   61 TyrLysThrSerPheHisAlaLeuThrSerIleLeuLysAlaGluGlyLeuArgGlyIle      80

Qy  352 TACACTGGGCTGTGGCTCGGTGCTGGCTCACCTACACCACTACCCCGCCCTTGGC         411
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Db   81 TyrThrGlyLeuTrpLeuGlyAlaGlyLeuLeuArgGlnAlaThrPheValGlyLeuGly     100

Qy  412 ATCTATACCGTGCTGTTTGAGCGGCTACTGGGGCTCACCCCGGCTTTCTG        471
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Qy  472 CTGAAGGCTGTGATTGGCATGAACCGCAGCGTGCCACTGGTCTTTGTGGAGCACACCACC     531
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Qy  532 GAAGTGGGCTCTTATCCGGATGACTGCCGATGGGGCCGGGCCACCTGGTGCCTTTGTGGGA    591
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Db  141 GluValAlaLeuIleArgMetThrAlaAspGlyArgLeuProLysAspGlyTyrArgGly     160

Qy  592 TACAAAAATGTGTTAACCGCCCTGAATTCGAATCACACCCGGGAGAGGGTGTCCTCACACTG   651
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Db  161 TyrLysAsnValPheAsnAlaLeuIleArgIleThrArgGluGluGlyValLeuThrLeu      180

Qy  652 TGGCGGGGCTGCATCCCTACCAGTGGCTTCGGGGTGCGTCAATGCTGGCTCGCC         711
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Db  181 TrpArgGlyCysIleProThrMetAlaArgAlaValValAlaAsnAlaAlaGlnLeuAla     200

Qy  712 TCCTACTCCCAATCCAAGCAGTTCTTACTGGACTACAGGGCTACTTCTCGACAACATCTTG    771
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Db  201 SerTyrSerGlnSerLysGlnPheLeuLeuAspTyrArgAlaThrSerArgAspAsnIleLeu   220

Qy  772 TGCCACTTCTGTGCCAGCATGATCAGCGGGTCTTGTCACCACTGCCTCCATGCCTGTG    831
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Db  221 CysHisPheCysAlaSerMetIleSerGlyLeuValThrThrAlaAlaSerMetProVal    240

Qy  832 GACATTGCCAAGACCCGAATCAGAGAACATGCGGATGATGGGAAGCCGGAATACAAAG     891
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Db  241 AspIleAlaLysThrArgIleArgGluHisAlaAspAspGlyLysProGluTyrLys      260

Qy  892 AACGGGGCTGAAGCGTGCTCGTTCAAAGTTGTCCGGTAACAGAGGGCGTTCTTCAGCCTGTGGAAG  951
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Db  261 AsnGlyLeuValLeuPheLysValValAlaArgTyrGluGlyPhePheSerLeuTrpLys      280

Qy  952 GGCTTCAGCGGCGTACTATCCCCGGCGGCCCCACACCGGTCCTCATCCTTCTG      1011
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Db  281 GlyPheThrProTyrTyrAlaArgLeuGlyProHisThrValLeuThrPheIlePheLeu        300

Qy 1012 GAGCAGGATGAACAAGGCCTACAAGGCGTCTTCCTCCAGTGGC                     1053
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RESULT 2
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; Sequence 3015, Application US/10/408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
;   APPLICANT:  Ghosh, Soumitra S.
;   APPLICANT:  Fahy, Eoin D.
;   APPLICANT:  Zhang, Bing
;   APPLICANT:  Gibson, Bradford W.
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OM nucleic - protein search, using frame_plus_n2p model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

Run on: February 1, 2006, 14:43:32 ; Search time 1.88877 Seconds
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1723.464 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 151242

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SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	554	19.5	313	7	US-11-010-239-109	Sequence 109, App
2	438.5	15.4	307	7	US-11-019-711-87	Sequence 87, Appl
3	430.5	15.1	307	7	US-11-019-711-88	Sequence 88, Appl
4	415.5	14.6	307	7	US-11-019-711-91	Sequence 91, Appl
5	407	14.3	306	7	US-11-019-711-89	Sequence 89, Appl
6	400	14.0	306	7	US-11-019-711-90	Sequence 90, Appl
7	387.5	13.6	306	7	US-10-063-703-126	Sequence 126, App
8	387.5	13.6	323	6	US-11-102-240-126	Sequence 126, App
9	344.5	12.1	271	7	US-11-010-239-109	Sequence 26, Appl
10	232	8.1	475	6	US-10-055-877-301	Sequence 301, Appl
11	213	7.5	469	6	US-10-063-703-58	Sequence 58, Appl
12	213	7.5	469	7	US-11-102-240-58	Sequence 58, Appl
13	213	7.5	568	6	US-10-055-877-300	Sequence 300, App
14	210	7.4	568	6	US-10-055-877-302	Sequence 302, App
15	209	7.3	384	6	US-10-055-877-299	Sequence 299, App
16	201	7.1	468	6	US-10-055-877-101	Sequence 101, App
17	199	7.0	308	6	US-09-978-360A-423	Sequence 423, App
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19	151	5.3	843	7	US-11-129-104-89	Sequence 89, Appl
20	148.5	5.2	482	7	US-11-055-877-298	Sequence 298, App
21	143	5.0	96	7	US-11-019-711-92	Sequence 92, Appl
22	143	5.0	96	7	US-11-019-711-93	Sequence 93, Ap
23	131.5	4.6	1970	7	US-11-149-003-20	Sequence 20, Appl
24	129	4.5	1207	6	US-10-995-561-990	Sequence 990, App
c 25	129	4.5	2102	6	US-10-995-561-989	Sequence 989, App
c 26	129	4.5	2108	6	US-10-995-561-991	Sequence 991, App
c 27	129	4.5	2157	6	US-11-000-463-243	Sequence 243, Appl
c 28	126	4.4	1464	6	US-11-186-284-28	Sequence 28, Appl
c 29	126	4.4	1464	7	US-11-021-603-2	Sequence 2, Appli
c 30	126	4.4	1464	7	US-11-021-603-2	Sequence 2, Appli
c 31	126	4.4	1467	6	US-10-821-234-1096	Sequence 1096, Ap
c 32	126	4.4	602	6	US-10-453-372-1064	Sequence 1064, Ap
c 33	125.5	4.4	1192	7	US-11-149-003-18	Sequence 18, Appl
c 34	125.5	4.4	1593	7	US-11-149-003-4	Sequence 4, Appli
c 35	124.5	4.4	3714	6	US-11-149-003-16	Sequence 16, Appli
c 36	124	4.4	1251	7	US-10-995-561-1015	Sequence 1015, Ap
c 37	123	4.4	1236	7	US-11-080-991-68	Sequence 68, Appl
c 38	122.5	4.3	1466	7	US-11-186-284-33	Sequence 33, Appli
c 39	122.5	4.3	1477	7	US-11-149-003-8	Sequence 8, Appli
40	122.5	4.3	1535	7	US-11-149-003-14	Sequence 14, Appl
41	122.5	4.3	1570	7	US-11-149-003-12	Sequence 12, Appl
42	122	4.3	1454	7	US-11-109-157A-2	Sequence 2, Appli
43	122	4.3	1566	6	US-10-453-372-1190	Sequence 1190, Ap
44	122	4.3	1686	7	US-11-109-157A-1	Sequence 1, Appli
c 45	122	4.3	1767	6	US-10-995-561-911	Sequence 911, App

ALIGNMENTS

RESULT 1
US-11-010-239-109
Sequence 109, Application US/11010239
Publication No. US20060015970A1
GENERAL INFORMATION:
APPLICANT: Roger PENNELL
APPLICANT: Jack OKAMURO
APPLICANT: Richard SCHNEEBERGER
APPLICANT: Yiwen FANG
APPLICANT: Shing KWOK
APPLICANT: Diane JOFUKU
APPLICANT: Edward A. KIEGLE
APPLICANT: Jonathan DONSON
APPLICANT: Nestor APUYA
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR
TITLE OF INVENTION: MODIFYING PLANT CHARACTERISTICS
FILE REFERENCE: 2750-1585PUS2
CURRENT APPLICATION NUMBER: US/11/010,239
CURRENT FILING DATE: 2004-12-09
PRIOR APPLICATION NUMBER: US 60/529,352
PRIOR FILING DATE: 2003-12-12
NUMBER OF SEQ ID NOS: 133
SOFTWARE: PatentIn version 3.3
SEQ ID NO 109
LENGTH: 313
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(313)
OTHER INFORMATION: 12395532_protein_ID_12395534
US-11-010-239-109

Alignment Scores:
Pred. No.:
Score: 9.87e-33
Percent Similarity: 554.00
Best Local Similarity: 55.7%
Query Match: 40.4%
DB: 19.5%
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US-09-888-264-2 (1-1503) x US-11-010-239-109 (1-313)

Length: 313
Matches: 124
Conservative: 47
Mismatches: 106
Indels: 30
Gaps: 3

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Qy  184 TTCCTTGTTTGGGGGCCTGGCCCGGGATGGGGAGCTACAGTTTTTGTCCAGCCCCTTGGACCTG 243
            |||||::||
Db    6 PheValGluGlyGlyIleAlaSerValIleAlaGlyCysSerThrHisProLeuAspLeu      25

Qy  244 GTGAAGAACCGGATGCAGTTGAGCGGGGGAAGGGGCCAAGACT------------           285
           |::||
Db   26 IleLysValArgLeuGlnLeuHisGlyGluAlaProSerThrThrThrValThrLeuLeu      45

Qy  286 ---------------CGGAGAGTACAAAAACCAGCTTCCATGCCCTCACCAGT---          321
                :::||||
Db   46 ArgProAlaLeuAlaPheProAsnSerSerProAlaAlaPheLeuGluThrThrSerSer      65

Qy  322 ------------------ATCCTGAAGGCAGGAAGGCCTGAGG                      345
                            |||
Db   66 ValProLysValGlyProIleSerLeuGlyIleAsnIleValLysSerGluGlyAlaAla      85

Qy  346 GGCATTTACAACTGGGGCGTGTCGGGGGCTGGCCTGGCCTCAGGCCACCTACACCACTACCCCG 405
           :::|||
Db   86 AlaLeuPheSerGlyValSerAlaThrLeuLeuArgGlnThrHisLeuTyrSerThrThrArg   105

Qy  406 CTTGGACACTATACCGGTGTTGAGGCGGCCTGACCTGGGGTGACTACTCCCCCCTGGC        465
           :::||||:||:|||
Db  106 MetGlyLeuTyrGluValValLeuLeuLysAsnGlyTrpThrAspProGluSerGlyLysLeuAsn 125

Qy  466 TTTCTGGCTTGGAAGGCTGTGATTGGCCATGACCGCGCAGGTGCCACTGGGTGCCTTTGTGGGAACA 525
           |||
Db  126 LeuSerArgLysIleGlyLeuValAlaGlyLysGlyGlyIleGlyTyrAlaAlaAlaValGlyAsn  145

Qy  526 CCAGCCGAAGTGGGCTCTTATCCGGCATGACTGCCGATGGGCCGGCTTCCAGCTGACCAGCGCC    585
           |||||
Db  146 ProAlaAspValAlaMetValArgMetGlnAlaAspGlyArgLeuProLeuAlaGlnArg       165

Qy  586 CGTGGCTACAAAAAATGTGTTTAACGGCCCCTGATTCGAATCACCCGGGAGAGAGGGTGTTCTC   645
           ||||||
Db  166 ArgGlnAsnTyrAlaGlyValGlyAspAlaIleAlaArgSerMetValLysGlyCysGlyValThr 185

Qy  646 ACACTGTGGCGCGGGGGCTGCATCCCTACCCATGGCTCGGGCGCCGTCGTCAAATGCTGCCCAG   705
           :::|||||:|:::||||
Db  186 SerLeuTrpArgGlySerAlaLeuThrIleAsnArgAlaMetIleValThrValThrAlaAlaGln 205

Qy  706 CTCGGCCTCCTACTCCCAATCCAAGCACAGTTCTTACTGGGACTACAGCTACTTCTCTGACAAC   765
           |||||||
Db  206 LeuAlaSerTyrAspGluGlyIleLeuGluGlnValAlaMetAsnAspGly                225

Qy  766 ATCTTGTGCCCACTTCTGTGTGCCACGATCAGGCGGTCTTGTTGTCCACCACTGCTGCTCATG    825
           :::
Db  226 LeuGlyThrHisValValAlaSerPheAlaLaAlaGlyPheValAlaSerValAlaSerAsn     245

Qy  826 CCTGTGGACAATGCCAAGACCCGAATCCAGACACATGCGGATGATTGATGGGGGAAGCCGGAA    885
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Db  246 ProValAspValIleLeuLysThrArgValMetAsnMetLysVal----------GlyAla     261

Qy  886 TACAAGAACGGGGCTGGACCTGCTGTTCAAAGTGTCCGCTACGAGGGCTTCTTCAGCCTG      945
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Db  262 TyrAsnGlyAlaTrpAspCysAlaLaValLysGluGlyAlaMetAlaLeu               281

Qy  946 TGGAAAGGCGCTTCACGCGCGCCGCCCCACACCGGTCCTCACCTTCATC               1005
           |||
Db  282 TyrLysGlyPheValProPheThrValCysArgGlnGlyProPheThrValValLeuPheVal   301

Qy 1006 TTCTTGGAGCAGATGAACAAG                                            1026
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Db  302 ThrLeuGluGlnValAlaArgLys                                          308
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Alignment Scores:
Pred. No.:
Score: 1.78e-24
Percent Similarity: 438.50
Best Local Similarity: 50.8%
Query Match: 32.8%
DB: 15.4%
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Length: 307
Matches: 98
Conservative: 54
Mismatches: 138
Indels: 9
Gaps: 4

US-09-888-264-2 (1-1503) x US-11-019-711-87 (1-307)

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                          GenCore version 5.1.7
                          Copyright (c) 1993 - 2006  Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:          February 2, 2006, 00:52:24  ; Search time 6638.73 Seconds
                                               (without alignments)
                                              10592.541 Million cell updates/sec

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Perfect score:   1503
Sequence:        1 cctcgtgccaggcgtgcgcg..........ccaaaaaaaaaaaaaaaaaa 1503
Scoring table:   IDENTITY NUC
                 Gapop 10.0 , Gapext 1.0
Searched:        41078325 seqs, 2339541228 residues
Total number of hits satisfying chosen parameters:    82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       EST:*
                 1: gb_est1:*
                 2: gb_est2:*
                 3: gb_est3:*
                 4: gb_htc:*
                 5: gb_est4:*
                 6: gb_est5:*
                 7: gb_est6:*
                 8: gb_est7:*
                 9: gb_gss1:*
                10: gb_gss2:*
                11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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                          %
Result          Query
No.    Score   Match  Length  DB  ID         Description
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   1  1459.4   97.1    1479    4  CR595953   CR595953 full-leng
   2  1457.4   97.0    1532    4  CR609603   CR609603 full-leng
 3  1456.4   96.9    1529    4  CR598517   CR598517 full-leng
   4  1444.4   96.1    1488    4  CR591200   CR591200 full-leng
   5  1441.4   95.9    1477    4  CR617034   CR617034 full-leng
   6  1427.4   94.7    1429    4  CR620583   CR620583 full-leng
   7  1423.4   94.7    1467    4  CR603391   CR603391 full-leng
   8  1408    93.7    1515    4  CR617848   CR617848 full-leng
   9  1384.4   92.1    1386    4  CR606322   CR606322 full-leng
  10  1381    91.9    1432    4  CR857161   CR857161 Pongo pyg
  11  1369    91.1    1369    4  CR590793   CR590793 full-leng
  12  1369    91.1    1369    4  CR590943   CR590943 full-leng
  13  1358    90.4    1358    4  CR625556   CR625556 full-leng
  14  1354    90.1    1354    4  CR613184   CR613184 full-leng
  15  1345    89.5    1345    4  CR615026   CR615026 full-leng
  16  1302    86.6    1302    4  CR613107   CR613107 full-leng
  17  1269.4   84.5    1271    4  CR600572   CR600572 full-leng
  18  1199    79.8    1199    4  CR625483   CR625483 Homo sapi
  19  1197.4   79.7    1199    4  BC016473   BC016473 Homo sapi
  20  1111    73.9    1122    4  CR591304   CR591304 full-leng
  21  1065.6   70.9    1147    5  BX395987   BX395987 full-leng
c 22  1063.6   70.8    1201    5  BX395986   BX395986 full-leng
  23  1051     69.9    1051    4  CR616117   CR616117 full-leng
c 24  1013.4   67.4    1174    5  BX424850   BX424850 full-leng
  25  1010.4   67.2    1201    1  AL529559   AL529559 full-leng
  26    990.2   66.1    1634    4  AK009487   AK009487 Mus muscu
c 27    990.2   65.9    1201    4  AL563855   AL563855 Mus muscu
  28    988.2   65.7    1464    4  AK009824   AK009824 Mus muscu
  29    986.6   65.6    1159    4  AL529560   AL529560 full-leng
  30    975.2   64.9    1165    1  AL547659   AL547659 full-leng
c 31    962.8   64.1    1120    1  AL529605   AL529605 full-leng
  32    960.6   63.9    1121    1  AL530824   AL530824 full-leng
  33    959.8   63.9    1058    1  BX333400   BX333400 full-leng
  34    953.6   63.4    1087    4  BX463231   BX463231 full-leng
  35    953.4   63.4    1125    1  AL519985   AL519985 full-leng
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  37    945      62.9    945     1  AY415734   AY415734 Homo sapi
  38    931.4   62.0    1053    1  AL572527   AL572527 full-leng
c 39    928.4   61.8    1188    1  AL529604   AL529604 full-leng
  40    920.2   61.2    1117    5  BX381492   BX381492 full-leng
c 41    918.4   61.1    1073    1  AL519984   AL519984 full-leng
c 42    914.2   60.8    1043    5  BX400267   BX400267 full-leng
  43    913.6   60.8    1141    5  BX394275   BX394275 full-leng
c 44    912.6   60.7    1049    5  BX363652   BX363652 full-leng
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ALIGNMENTS

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LOCUS       CR595953                1479 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DD014YH08 of T cells (Jurkat cell line)
            Cot 10-normalized of Homo sapiens (human).
ACCESSION   CR595953
VERSION     CR595953.1  GI:50476760
KEYWORDS    HTC; CNSLT cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1479)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1479)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1..1479
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DJ014YH08"
                     /tissue_type="T cells (Jurkat cell line) Cot
                     10-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

Query Match      97.1%;  Score 1459.4;  DB 4;  Length 1479;
Best Local Similarity  99.9%;  Pred. No. 0;
Matches 1460; Conservative  0; Mismatches  1;  Indels  0;  Gaps  0;
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Qy    11 GGGCGTGCGCGGCGCCCTCGCTCTGTTGTGCGGCGGTGTCACCTTGGGCGGGCGGAGCGGGGGC       70
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Db    19 GGGCGTGCGCGGCGCCCCTCGCTCGTTGTGCGGGGGGTGTCACCTTGGGCGGGCGGGAGCGGGGGCC    78

Qy    71 GTGCGCGCCACGCGGCGCACCCCGAGCCGAGCGGGGCCATTGAGTGGCGATGGCGGACGGAGTG     130
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    79 GCGCGCGCCACGCGGCGACCCCGAGCGGAGCGGGGCCATTGAGTGGCGATGGCGGACGGAGTG     138

Qy   131 CCCGGGCCGGCGGGATAGACGGGGAAGCCCGGGCTACCTCGGTCGGTCGTCAAGTTCCTGT     190
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   139 CCCGGGCCGGCGGGATAGACGGGGAAGCCCGGGCTACCTCGGTCGGTCGTCAAGTTCCTGT     198

Qy   191 TTGGGGGCCTGGGCGGGGACGGGGAGCTACAGTTTTTGTCCAGCCCTGGTTGTGAGA     250
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   199 TTGGGGGCCTGGGCGGGGATGGGGAGCTACAGTTTTTGTCCAGCCCTGGTTGTGAGA     258

Qy   251 ACCGGATGCAGTTGAGCGCGGGAGGGCCAAGACTCGAGAGTACAAAACCAGCTTCCATG     310
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Db   259 ACCGGATGCAGTTGAGCGCGGGAGGGCCAAGACTCGAGAGTACAAAACCAGCTTCCATG     318

Qy   311 CCCTCACCAGTATCCTGAAGGCAGAAGGCCTGAGGGGGCATTACACTCGGGCTGTG     370
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Db   319 CCCTCACCAGTATCCTGAAGGCAGAAGGCCTGAGGGGGCATTACACTCGGGCTGTG     378

Qy   371 GCCTGGCTCCGTCAGGCCACCTACCACCACTCTATACCGTTGTTTG     430
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Db   379 GCCTGCTCCGTCAGGCCACCTACCACCACTCTATACCGTTGTTTG     438

Qy   431 ACGGCCTTGACTGGGGATGGGGGTACTCCCCCTGGCTTTCTCCTTGAAGGCTGTGATTGGCA     490
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   439 AGCGGCCTGACTGGGGATGGGGGTACTCCCCCTGGCTTTCTCGTGAAGGCTGTGATTGGCA     498

Qy   491 TGACCGCAGGTGCCACTGGTGCCTTTGTGGGGACCAGCGGAAGTGGCTCTTATCCGCA     550
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Db   499 TGACCGCAGGTGCCACTCGTGCCTTTGTGGGGACCAGCGGAAGTGGCTCTTATCCGCA     558

Qy   551 TGACTGCCATGGCCGGGCTTCCAGCTGACCAGCGCCGTGCTACAAAAAATGTGTTTAACG     610
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Db   559 TGACTGCCGATGGCCGGGCTTCCAGCTGACCAGCGCCGTGCTACAAAAAATGTGTTTAACG     618

Qy   611 CCCTGATTCGAATCACCCGGGAAGAGGGGTGTCTCACACTGTGCGGCGGCTTGCATCCCTA     670
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Db   619 CCCTGATTCGAATCACCCGGGAAGAGGGGTGTCCTCACACTGTGCGGCTGCATCCCTA     678

Qy   671 CCATGGCTCGGGGCCGTCGGTCGTCAAATGCTGCCCAGCTGCCCTCCTACTCCCAATCCAAGC     730
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Db   679 CCATGGCTCGGGGCCGTCGTCGTCAAATGCTGCCCAGCTGCCCTCCTACTCCCAATCCAAGC     738

Qy   731 AGTTCTTACTGGACTCACTCCTTCTCTGACAACATCTTGTGCCACTTCTGTGCCACGA     790
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Db   739 AGTTCTTACTGGACTCACTCCTTCTCTGACAACATCTTGTGCCACTTCTGTGCCACCA     798

Qy   791 TGATCAGCGGGTCTTGTTCACCACTGGCTGCCTCCATGCCTGTGACCTGGACACCCGAA     850
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Db   799 TGATCAGCGGGTCTTGTTCACCACTGGCTGCCTCCATGCCTGTGAGACCCGAA     858

Qy   851 TCCAGAACATGCGGATGATGATGGGGAAGCCGGAATACAAGAACACGGGCTGGAGGTTGCTGT     910
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   859 TCCAGAACATGCGGATGATGATGGGGAAGCCGGAATACAAGAACACGGGCTGGAGGTTGCTGT     918

Qy   911 TCAAAGTTGTCCGCTACAGAGAGGGGCTTCACGCGGCCGTTGACGGTTACTATG     970
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   919 TCAAAGTTGTCCGCTACAGAGGGGCTTCCAGGGGCTTCACGCGGCCGTTACTATG     978

Qy   971 CCCGGCCTGGGCCCCCACACCGTCCTCACTTCACTTCTCTTGGAGCAGATGAACAAGGCCT     1030
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Db   979 CCCGGCCTGGGCCCCCACACCGTCCTCACTTCACTTCTCTTGGAGCAGATGAACAAGGCCT     1038

Qy  1031 ACAAAGCGTCTCTTCCTCAGTGGGTGAAGGCTCCCACTCGGCCTGCTGCTGCGGCGCCT     1090
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Db  1039 ACAAAGCGTCTTCCTCAGTGGGTGAAGGCGCTCCCACTCGGCCTGCTGCTGCGGCGCCT     1098

Qy  1091 ATAGCCACTCGCCCTGGGGGGCCTGGGGCTCGGGCTGGCCTGCCCGGGAGACCCCCTCGATTTATTTCCC     1150
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1099 ATAGCCACTCGCCCTGGGGGGCCTGGGGCTCGGGCTGGCCTGCCCGGGAGACCCCCTCGATTTATTTCCC    1158

Qy  1151 TTCCACAGTGTGGTTTCTTCCTCTGCGGTAAAGGCACTTGGTCTGTCTCTTCTACCCCTCC     1210
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Db  1159 TTCCACAGTGTGGTTTCTTCCTCTGCGGTAAAGGGACTTGGTCTGTCTGTTCTACCCCTCC    1218

Qy  1211 AGCTTGCCCTGCTCGTCCTTGATCCTGTGATTCTCTGCGGTATTCTTGGTCGTATTCTTGCAGGGAG     1270
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Db  1219 AGCTTGCCCTGCTCGTCCTTGATCCTGTGATTCTCTGCGGTATTCTTGGTCGTATTCTTGCAGGGAG    1278

Qy  1271 CTGGAAAACTTCCTGAGGATTCTGGCCTGCCCCTCCCCCCTCGGGTTTAGTTCAGGGCGCACAGG     1330
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1279 CTGGAAAACTTCCTGAGGATTTCAGTGGGGCGGCCCTCCCCCTGGGGTTTTAGTTCAGGGCACACAGG    1338

Qy  1331 ACAGCAGAAGATCCCCTTTGTCAGTGGGGAAAACCAAGGACAGCAGGGAGAGACAGGGAGG     1390
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Db  1339 ACAGCAGAAGATCCCCTTTGTCAGTGGGGGAAAACCAAGGACAGCAGGGAGAGACAGGGAGG    1398

Qy  1391 AGCAGAAGCCATCAAGATGGTCAAAAGGGGCCTGCAGGGGAGAGATGTGGCCCTTCTCCCCC     1450
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Db  1399 AGCAGAAGCCATCAAGATGGTCAAAAGGGGCCTGCAGGGGAGAGATGTGGCCCTTCTCCCCC    1458

Qy  1451 TCATTGAGGACTTAATAAATT     1471
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Db  1459 TCATTGAGGACTTAATAAATT    1479
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RESULT 2
CR609603

LOCUS	CR609603 1532 bp mRNA linear HTC 21-JUL-2004
DEFINITION	full-length cDNA clone CS0DC010YO07 of Neuroblastoma Cot 25-normalized of Homo sapiens (human).
ACCESSION	CR609603
VERSION	CR609603.1 GI:50490410
KEYWORDS	HTC; CNSLT_cDNA.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 1532)
AUTHORS	Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL; http://fullength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue
REFERENCE	2 (bases 1 to 1532)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage ; BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT	- Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

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ORIGIN	

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Best Local Similarity 99.9%;
Matches 1458;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2006, 21:01:47 ; Search time 7900.19 Seconds
(without alignments)
10814.381 Million cell updates/sec

Title: US-09-888-264-2
Perfect score: 1503
Sequence: 1 cctcgtgccaggcggtgcgcg..........ccaaaaaaaaaaaaaaaa 1503

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 2842172565 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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            8: gb_pr:*
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           13: gb_vi:*
           14: gb_htg:*
           15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1503	100.0	1503	6	CQ904292	CQ904292 Sequence
2	1503	100.0	1503	8	AF070548	AF070548 Homo sapi
3	1488.2	99.0	1561	8	BC017170	BC017170 Homo sapi
4	1488.2	99.0	1562	8	BC006508	BC006508 Homo sapi
5	1488.2	99.0	1562	8	BC006519	BC006519 Homo sapi
6	1488.2	99.0	1570	8	AX840916	AX840916 Sequence
7	1424.2	94.8	1434	6	CQ769639	CQ769639 Sequence
8	1422	94.6	1422	6	BC016294	BC016294 Homo sapi
9	1015	67.5	1454	4	M60662	M60662 Bovine 2-ox
10	1014.8	67.5	1555	9	BOVOMCPB	BOVOMCPB Bovine
11	1002.4	66.7	1652	9	BC003455	BC003455 Mus muscu
12	973.8	64.8	1403	4	BC019631	BC019631 Mus muscu
13	971.8	64.7	1124	6	BT020806	BT020806 Bos tauru
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18	784	52.2	946	9	RNU84727	U84727 Rattus norv
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c	21	600.4	39.9	181825	8	AC109333	AC109333 Homo sapi
c	22	590	39.3	1396	7	BC093472	BC093472 Xenopus t
c	23	588.4	39.1	91927	8	AC004771	AC004771 Homo sapi
c	24	587	39.1	129169	14	AC032038	AC032038 Homo sapi
c	25	579	38.5	1349	5	BC072308	BC072308 Xenopus l
c	26	544.2	36.2	2371	4	BT2OXOC	BT2OXOC Danio rer
c	27	523.8	34.9	1697	5	BC071521	BC071521 Danio rer
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c	29	396.6	26.4	1290	2	AK114270	AK114270 Ciona int
c	30	356.6	23.7	1654	6	CQ573057	CQ573057 Sequence
c	31	353.4	23.5	1672	2	AY052135	AY052135 Drosophil
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c	33	314.6	20.9	68487	14	AC017782	AC017782 Drosophil
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c	35	314.6	20.9	178791	2	AC008218	AC008218 Drosophil
c	36	314.6	20.9	224264	2	AE003770	AE003770 Drosophil
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c	38	291.2	19.4	196708	14	AC116247	AC116247 Rattus no
c	39	291.2	19.4	263882	14	AC107344	AC107344 Rattus no
c	40	285.4	19.0	319	4	AF233352	AF233352 Ovis arie
c	41	274.6	18.3	194230	9	CR933736	CR933736 Mouse DNA
c	42	274.6	18.3	194609	14	AC013775	AC013775 Mus muscu
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ALIGNMENTS

RESULT 1
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LOCUS       CQ904292       1503 bp    DNA     linear   PAT 16-NOV-2004
DEFINITION  Sequence 2 from Patent EP1475439.
ACCESSION   CQ904292
VERSION     CQ904292.1  GI:55785556
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Adams,S. and Yu,X.X.
  TITLE     Control of metabolism with compositions of the human 2-oxoglutarate
            carrier
  JOURNAL   Patent: EP 1475439-A 2 10-NOV-2004;
            Genentech, Inc. (US)
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Matches 1503;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy     61 GAGCGGGGGGCCGGTGCGCGCCCACGGGGACCCCGAGCCGGCCATTGAGTGGCGGATGGCGCG 120
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Qy    121 ACGGCGCGAGTGCCGGGGCCGGGGCCCGGGGATAGACGGGAAGCCCCGTACCTCCCCTAAGTCCGTC 180
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Qy   181 AAGTTTCCTGTTTGGGGGCCGGATGGGGGGGAGCTACAGTGTTTTTGTGTCCAGCCCCTGAC 240
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Qy   241 CTGGTGAAGAACCGGATGCAGTTGAGCGCGGGAAGGGGCCAAGACTCGGAGGTACAAAACC 300
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Db   241 CTGGTGAAGAACCGGATGCAGTTGAGCGCGGGGAAGGGGCCAAGACTCGGAGGTACAAAACC 300

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Qy   361 CTGTCGGGGCTGGGCCTGCTGCTGCTCAGGCAGCCACCTACATCTATACC 420
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Qy   721 CAATCCAAGCAGTTCTTACTGGACTCAGGCTACTTCTCTGACAACATCTTGTTGTCCCACTTC 780
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Qy  1021 AACAAGGCCTACAAGGCGTCTCTCCTCACCATCACCGTCCTCACTTCATCTTCTTGGAGCAGATG 1080
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Qy  1201 CCCCTGCTTCCCAGTTGCCCTCGTCGTCTTGATCTGTGATTTCTGTCTTGGCTATTC 1260
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Qy  1381 GACAGGGGAGGAAGCCATCAAGATCGGTCAAAAGGGGCTGCAGGGAGATCGTGGGCCC 1440
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Qy  1441 TTCCTCCCCTCATTGAGGACTTAATAAATTGGATTGATGACACCCAAAAAAAAAAAAA 1500
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Qy  1501 AAA 1503
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Db  1501 AAA 1503
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RESULT 2
AF070548

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LOCUS       AF070548              1503 bp    mRNA    linear   PRI 05-AUG-1998
DEFINITION  Homo sapiens clone 24408 2-oxoglutarate carrier protein mRNA,
            complete cds.
ACCESSION   AF070548
VERSION     AF070548.1  GI:3387910
KEYWORDS    FLI_CDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1503)
  AUTHORS   Andersson,B., Wentland,M.A., Ricafrente,J.Y., Liu,W. and Gibbs,R.A.
  TITLE     A 'double adaptor' method for improved shotgun library construction
  JOURNAL   Anal. Biochem. 236 (1), 107-113 (1996)
  PUBMED    8619474
REFERENCE   2  (bases 1 to 1503)
  AUTHORS   Yu,W., Andersson,B., Worley,K.C., Muzny,D.M., Ding,Y., Liu,W.,
            Ricafrente,J.Y., Wentland,M.A., Lennon,G. and Gibbs,R.A.
  TITLE     Large-scale concatenation cDNA sequencing
  JOURNAL   Genome Res. 7 (4), 353-358 (1997)
  PUBMED    9110174
REFERENCE   3  (bases 1 to 1503)
  AUTHORS   Yu,W. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JUN-1998) Molecular and Human Genetics, Baylor
            College of Medicine, One Baylor Plaza S930, Houston, TX 77030, USA
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                     /tissue_type="brain"
                     /clone_lib="INIB"
                     /dev_stage="infant"
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                     SLWKGFPPYARLGPHVLTLTIFLBQMNKAYRLFLSG"
ORIGIN
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                GenCore version 5.1.7
        Copyright (c) 1993 - 2006  Biocceleration Ltd.
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2006, 20:32:32 ; Search time 980.441 Seconds
(without alignments)
10216.861 Million cell updates/sec

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Perfect score: 1503
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Scoring table: IDENTITY NUC
Searched: 4996997 seqs, 333246308 residues
Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 9993994

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0
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2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
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14: geneseqn2005s:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	Query Match %	Length	DB	ID	Description
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	2	1488.2	99.0	1570	10	ACH00820	Ach00820 Human sol
	3	1424.2	94.8	1434	10	ADI62922	Adi62922 Human apo
	4	1363.8	90.7	2586	10	ADC30801	Adc30801 Human nov
	5	1147.4	76.3	1466	12	ADJ27252	Adj27252 Human TRI
	6	968.0	64.4	1123	6	ABA93091	Aba93091 Human 2-o
	7	941.8	62.7	945	13	ADQ89939	Adq89939 Antagonis
	8	919	61.1	1098	12	ADJ27261	Adj27261 Human TRI
	9	824.2	54.8	1091	12	ADJ67689	Adj67689 Kif1C DNA
	10	784	52.2	946	10	ADB58443	Adb58443 Toxicity-
	11	784	52.2	946	12	ADP72899	Adp72899 Renal tox
	12	784	52.2	946	14	ADV41249	Adv41249 Rat cardi
	13	784	52.2	946	14	ADZ60768	Adz60768 Rat LOC64
	14	648.4	43.1	947	13	ADN33186	Adn33186 Human tra
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c	16	554.6	36.9	613	10	ADD32951	Add32951 Human mit
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c	20	418.4	27.8	2122	13	ACN43708	Acn43708 Human dia
c	21	418.4	27.8	2268	13	ACN43706	Acn43706 Human dia
c	22	368.8	24.5	688	13	ADQ51456	Adq51456 Novel can
	23	362	24.1	418	9	ACH13741	Ach13741 Human adu
	24	359	23.9	454	9	ACH14565	Ach14565 Human adu
	25	356.6	23.7	1654	4	ABL02383	Abl02383 Drosophil
	26	353.4	23.5	366	10	ADD33132	Add33132 Human mit
c	27	353.4	23.5	366	10	ADK61375	Adk61375 Ovarian c
c	28	337.6	22.5	458	4	AAD17748	Aad17748 Human mac
	29	314.6	20.9	3725	4	ABL02382	Abl02382 Drosophil
	30	308.6	20.5	1205	13	ADX51274	Adx51274 Plant ful
c	31	274.6	18.3	24127	11	ACN44540	Acn44540 Mouse gen
	32	260	17.3	469	13	ADU18167	Adu18167 Periphera
	33	260	17.3	469	13	ADU11195	Adu11195 Solid tum
	34	260	17.3	469	13	ADU48191	Adu48191 Human SLC
	35	257.2	17.1	1398	14	ADY64719	Ady64719 S. manson
	36	253	16.8	1017	4	ABL20299	Abl20299 Drosophil
	37	253	16.8	3017	4	ABL20298	Abl20298 Drosophil
	38	249.8	16.6	906	4	ABL02209	Abl02209 Drosophil
	39	249.8	16.6	906	13	ADQ89737	Adq89737 Antagonis
	40	249.8	16.6	2906	4	ABL02208	Abl02208 Drosophil
c	41	194.4	12.9	1736	13	ACN43711	Acn43711 Human dia
c	42	194.4	12.9	2028	13	ACN43710	Acn43710 Human dia
c	43	194.4	12.9	2174	13	ACN43707	Acn43707 Human dia
c	44	188	12.5	188	10	ADF79982	Adf79982 Leukaemia
c	45	177	11.8	506	10	ADB55381	Adb55381 Toxicity-

ALIGNMENTS

RESULT 1
ABA93092

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ID   ABA93092 standard; cDNA; 1503 BP.
XX
AC   ABA93092;
XX
DT   12-APR-2002  (first entry)
XX
DE   Human 2-oxoglutarate carrier (OGC) cDNA sequence AF070548 SEQ ID NO:2.
XX
KW   Human; 2-oxoglutarate carrier; OGC; uncoupling protein; UCP; gene;
KW   immunosuppressive; immunomodulator; vulnerary; cerebroprotective;
KW   anorectic; obesity; cachexia; metabolic disorder; stroke; trauma; sepsis;
KW   infection; ss.
XX
OS   Homo sapiens.
XX
XX
PN   WO200198512-A2.
XX
PD   27-DEC-2001.
XX
PF   22-JUN-2000; 2001WO-US020020.
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PR   22-JUN-2000; 2000US-0213307P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Adams S, Yu XX;
XX
DR   WPI; 2002-130794/17.
XX
PT   Screening for compounds that affect uncoupling, useful for identifying
PT   human 2-oxoglutarate carrier (OGC) agonists or antagonists for treating
PT   obesity or cachexia, respectively, by analyzing the expression of human
PT   OGC within the sample.
XX
PS   Example 1; Page 26; 53pp; English.
XX
CC   The present invention describes a method of screening for compounds that
CC   affect uncoupling. The method comprises analysing the expression of a
CC   human 2-oxoglutarate carrier (OGC) protein within the sample. OGC has
CC   anorectic, immunomodulator, vulnerary, cerebroprotective and
```

```
CC   immunosuppressive activities. The method is useful for screening
CC   compounds that affect uncoupling, particularly OGC antagonists or
CC   agonists. The OGC agonist is particularly useful for increasing the
CC   metabolic rate in a mammal to treat obesity. The OGC antagonist is useful
CC   for treating cachexia. The method is also useful for detecting and
CC   treating metabolic disorders. Modulating the metabolic rate in a mammal
CC   has a variety of therapeutic applications, including treatment of obesity
CC   and the symptoms associated with stroke, trauma (e.g. burn trauma),
CC   sepsis or infection. OGC is an uncoupling protein. The present sequence
CC   represents a human OGC cDNA sequence used in the exemplification of the
CC   present invention, which is that of the GenBank accession number AF070548
XX
SQ   Sequence 1503 BP; 285 A; 451 C; 437 G; 330 T; 0 U; 0 Other;

Query Match      100.0%;    Score 1503;   DB 6;   Length 1503;
Best Local Similarity   100.0%;    Pred. No. 0;
Matches 1503;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;
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Qy       121 ACGGGCGAGTGCGCGGGGGGCGGGGGGGGGGGGATAGGACACGGGGGGGGC 180
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Qy       181 AAGTTCCTGTTTGGGGGGGCCTGGGCGGGGGGGGCTACAGTTTTTTGTCC 240
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Qy       241 CTGGTGAAGAACCGGATCGCAGTTGAGCGGGGGAAGGGGGCCAAGACTCG 300
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Qy      1441 TTCCTCCCCCTCATTGAGGACTTAATAAATTGGATTGATGACACCAAAAAAAAAAAAAAAA 1500
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Qy      1501 AAA 1503
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Db      1501 AAA 1503
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OM nucleic - nucleic search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on: February 2, 2006, 14:46:55 ; Search time 1355.33 Seconds
(without alignments)
9170.349 Million cell updates/sec

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Perfect score: 1503
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 413468905 residues
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1503	100.0	1503	3	US-09-888-264-2	Sequence 2, Appli
2	1488.2	99.0	1570	9	US-10-507-617-12	Sequence 12, Appl
3	968.6	64.4	1123	3	US-09-888-264-1	Sequence 1, Appli
4	941.8	62.7	945	10	US-10-745-237-369	Sequence 369, App
5	824.2	54.8	1091	7	US-10-261-175A-5	Sequence 5, Appli
6	784	52.2	946	7	US-10-191-803-147	Sequence 147, App
7	784	52.2	946	8	US-10-764-420-492	Sequence 492, App
8	600.4	39.9	14661	8	US-10-741-600-1748	Sequence 1748, A
9	600.4	39.9	17149	8	US-10-741-600-17980	Sequence 17980, A
10	600.4	39.9	24741	8	US-10-741-600-17979	Sequence 17979, A
11	600	39.9	14943	8	US-10-741-600-17979	Sequence 17979, A
12	588.4	39.1	8098	6	US-10-264-237-2856	Sequence 2856, A
13	449.6	29.9	473	6	US-09-918-995-20014	Sequence 20014, A
14	441.8	29.4	552	3	US-09-918-995-10779	Sequence 10779, A
15	362	24.1	418	3	US-09-918-995-953	Sequence 953, App
16	359	23.9	454	10	US-09-918-995-1777	Sequence 1777, Ap
17	356.6	23.7	1654	10	US-11-097-143-815	Sequence 815, App
18	353.4	23.5	366	9	US-10-505-680-545	Sequence 545, App
19	314.6	20.9	3725	10	US-10-425-114-26014	Sequence 26014, A
20	308.6	20.5	1205	8	US-10-425-115-26999	Sequence 26999, A
21	308.6	20.5	1207	8	US-10-087-192-1039	Sequence 1039, Ap
22	274.6	18.3	24127	8	US-10-793-032-14	Sequence 14, Appl
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25	253	16.8	3017	10	US-11-097-143-27688	Sequence 27688, A
26	249.8	16.6	906	9	US-10-745-237-167	Sequence 167, App
27	249.8	16.6	906	10	US-11-097-143-554	Sequence 554, App
28	249.8	16.6	2906	10	US-11-097-143-553	Sequence 553, App
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33	169.4	11.3	1898	7	US-10-425-114-6241	Sequence 6241, Ap
34	169.4	11.3	2201	7	US-10-424-599-133253	Sequence 133253,
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38	149	9.9	761	8	US-10-425-114-19049	Sequence 19049, A
39	143	9.5	761	8	US-10-425-115-118086	Sequence 118086,
40	142.2	9.5	1206	7	US-10-424-599-74777	Sequence 74777, A
41	141.6	9.4	1414	8	US-10-425-115-30789	Sequence 30789, A
42	140	9.3	1167	7	US-10-425-114-18168	Sequence 18168, A
43	140	9.3	1368	7	US-10-425-114-3304	Sequence 3304, Ap
44	140	9.3	1931	8	US-10-425-115-79538	Sequence 79538, A
45	138.4	9.2	1238	7	US-10-425-114-19387	Sequence 19387, A

ALIGNMENTS

RESULT 1
US-09-888-264-2

; Sequence 2, Application US/09888264
; Patent No. US20020103150A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Sean
; APPLICANT: Yu, Xiang Xian
; TITLE OF INVENTION: CONTROL OF METABOLISM WITH COMPOSITIONS OF THE HUMAN 2-OXOGLUTARA
; TITLE OF INVENTION: CARRIER
; FILE REFERENCE: 10466/35
; CURRENT APPLICATION NUMBER: US/09/888,264
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/213,307
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo sapiens; GenBank AF070548
US-09-888-264-2

Query Match 100.0%; Score 1503; DB 3; Length 1503;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1503; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 GAGCGGGGCGCCGTTGCGCGCACGGGAACCCGAGGGCCCATTGAGTGGCGATGGGGGCGCG 120
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RESULT 2
US-10-507-617-12

; Sequence 12, Application US/10507617
; Publication No. US20050119206A1
; GENERAL INFORMATION:
; APPLICANT: Eulenberg, Karsten
; APPLICANT: Steuernagel, Arnd
; APPLICANT: Haeder, Thomas
; APPLICANT: Broenner, Guenter
; TITLE OF INVENTION: CG8327, CG10823, CG18418, CG15862, CG3768, CG11447 and CG16750
; TITLE OF INVENTION: Homologous Proteins Involved in the Regulation of Energy
; TITLE OF INVENTION: Homeostasis
; FILE REFERENCE: 2923-651
; CURRENT APPLICATION NUMBER: US/10/507,617
; CURRENT FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: PCT/EP03/02714
; PRIOR APPLICATION FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: EP 02 005 882.2
; PRIOR APPLICATION FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: EP 002 006 012.5
; PRIOR APPLICATION FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: EP 02 006 271.7
; PRIOR APPLICATION FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: EP 02 006 810.2
; PRIOR APPLICATION FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 12
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-507-617-12

Query Match 99.0%; Score 1488.2; DB 9; Length 1570;
Best Local Similarity 99.8%; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Matches 1490;

(Sequence alignment data — Qy/Db nucleotide sequences, positions 11–1503 / 301–1503)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2006, 20:32:32 ; Search time 732.559 Seconds
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Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	968.6	86.3	1503	9	ABA93092	Aba93092 Human 2-o
4	968.6	86.3	1570	10	ACH00820	Ach00820 Human sol
5	945	84.1	945	13	ADQ89939	Adq89939 Antagonis
6	874.6	77.9	1098	12	ADJ27261	Adj27261 Human TRI
7	874.6	77.9	2586	10	ADC30801	Adc30801 Human nov
8	802.6	71.5	1091	12	ADJ67689	Adj67689 K1f1C DNA
9	787.2	70.1	946	13	ADB58443	Adb58443 Toxicity-
10	787.2	70.1	946	12	ADP72899	Adp72899 Renal tox
11	787.2	70.1	946	13	ADV41249	Adv41249 Rat cardi
12	787.2	70.1	946	14	ADZ60768	Adz60768 Rat LOC64
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19	337.4	30.0	2038	13	ACN43709	Acn43709 Human dia
20	337.4	30.0	2122	13	ACN43708	Acn43708 Human dia
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26	255.6	22.8	688	13	ADQ51456	Adq51456 Novel can
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39	142.4	12.7	366	10	ADD33132	Add33132 Human mit
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ALIGNMENTS

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AC   ABA93091;
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DT   12-APR-2002 (first entry)
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KW   anorectic; obesity; cachexia; metabolic disorder; stroke; trauma; sepsis;
KW   infection; ss.
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PD   27-DEC-2001.
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PF   22-JUN-2001; 2001WO-US020020.
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PR   22-JUN-2000; 2000US-0213307P.
XX
PA   (GETH) GENENTECH INC.
XX
PI   Adams S, Yu XX;
XX
DR   WPI; 2002-130794/17.
XX
PT   Screening for compounds that affect uncoupling, useful for identifying
PT   human 2-oxoglutarate carrier (OGC) agonists or antagonists for treating
PT   obesity or cachexia, respectively, by analyzing the expression of human
PT   OGC within the sample.
XX
PS   Example 1; Page 26; 53pp; English.
XX
CC   The present invention describes a method of screening for compounds that
CC   affect uncoupling. The method comprises analysing the expression of a
CC   human 2-oxoglutarate carrier (OGC) protein within the sample. OGC has
CC   anorectic, immunomodulator, vulnerary, cerebroprotective and

CC   immunosuppressive activities. The method is useful for screening
CC   compounds that affect uncoupling, particularly OGC antagonists or
CC   agonists. The OGC agonist is particularly useful for increasing the
CC   metabolic rate in a mammal to treat obesity. The OGC antagonist is useful
CC   for treating metabolic disorders. The method is also useful for detecting and
CC   treating metabolic cachexia. Modulating the metabolic rate in a mammal
CC   has a variety of therapeutic applications, including treatment of obesity
CC   and the symptoms associated with stroke, trauma (e.g. burn trauma),
CC   sepsis or infection. OGC is an uncoupling protein. The present sequence
CC   represents a human OGC cDNA sequence used in the exemplification of the
CC   present invention, which is that of the GenBank accession number
CC   NM_003562
XX
SQ   Sequence 1123 BP; 229 A; 330 C; 332 G; 232 T; 0 U; 0 Other;

Query Match   100.0%; Score 1123; DB 6; Length 1123;
Best Local Similarity   100.0%; Pred. No. 3.1e-283;
Matches 1123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   61 GGAAGCCCCGTACCTCCCCTAAGTCCGTCAAGTTCCTGTTTGGGGGCCGTG 120
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Qy   361 GTACTCCCCTGGCTTTCTGCTGAAGGCTGTGATTGGGCATGACCGCAGTGCCACTGGTTG 420
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Qy   841 GCTTCTTCAGCCCTGTGGAAGGGCTTCACCGCGGTACTACTATGCCGGCTA 900
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Qy   901 TCCTCACCTTCATCTTCTTGGAGCAGATGAACAAGGCCTACAAGGGTCTCTTTCCTCAGTG 960
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RESULT 2

AD162922
ID   AD162922 standard; cDNA; 1434 BP.
XX
AC   AD162922;
XX
DT   22-APR-2004 (first entry)
XX
DE   Human apoptosis-associated cDNA SEQ ID 365.
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KW   apoptosis; cell death; cytostatic; neuroprotective; immunosuppressive;
KW   antirheumatic; antiarthritic; dermatological; antiinflammatory;
KW   hepatotropic; virucide; nootropic; anticonvulsant; antiparkinsonian;
KW   vasotropic; cerebroprotective; antialcoholic; gene therapy; tumour;
KW   autoimmune disease; degenerative disease; viral infection; leukaemia;
KW   carcinoma; sarcoma; multiple sclerosis; rheumatoid arthritis; diabetes;
KW   lupus; hepatitis; influenza viruses; Alzheimer's disease;
KW   Huntington's disease; Parkinson's disease; reperfusion injury; stroke;
KW   alcoholic liver disease; human; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200305021-A2.
XX
PD   17-JUL-2003.
XX
DR   WPI; 2003-542134/51.
XX
PI   Koenig-Hoffman K, Kazinski M, Schaefer R, Keper B;
XX
PA   (XANT-) XANTOS BIOMEDICINE AG.
XX
PR   11-JAN-2002; 2002DE-01000856.
XX
PF   13-JAN-2003; 2003WO-EP000270.
XX
PT   New nucleic acids involved in apoptosis, useful for diagnosis and
PT   treatment of e.g. tumors and degenerative disease, also related proteins,
PT   antibodies and modulators.
XX
PS   Claim 1b; SEQ ID NO 365; 517pp; German.
XX
CC   This invention describes novel nucleic acid molecules that are associated
CC   with apoptosis and encode a polypeptide and are derived from a normalised
CC   gene library (embryonic or liver) or clone collections, and the extent of
CC   apoptosis measured by cell death detection assay or the CPRG assay
CC   (measuring loss of membrane integrity). The products of the invention
CC   have cytostatic, neuroprotective, immunosuppressive, antirheumatic,
CC   antiarthritic, dermatological, antiinflammatory, hepatotropic, virucide,
CC   nootropic, anticonvulsant, antiparkinsonian, vasotropic,

OM nucleic - nucleic search, using sw model

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Searched: 5883141 seqs, 2842172S653 residues

Total number of hits satisfying chosen parameters: 11766282

Post-processing: Minimum Match 0%
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1107.2	98.6	1124	8	CQ725283	CQ725283 Sequence
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8	968.6	86.3	1562	8	BC006508	BC006508 Homo sapi
9	968.6	86.3	1562	8	BC006519	BC006519 Homo sapi
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14	857	76.3	1454	4	BOVOMCPB	BOVOMCPB Bovine 2-ox
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40  254.6  22.7 29183  14  CQ599931  CQ599931 Sequence
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ALIGNMENTS

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DEFINITION  Sequence 1 from Patent EP1475439.
ACCESSION   CQ904291
VERSION     CQ904291.1  GI:55785555
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS     Adams,S. and Yu,X.X.
TITLE       Control of metabolism with compositions of the human 2-oxoglutarate
            carrier
JOURNAL     Patent: EP 1475439-A 1 10-NOV-2004;
            Genentech, Inc. (US)
FEATURES            Location/Qualifiers
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Best Local Similarity   100.0%;
Matches 1123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION   Sequence 11217 from Patent WO02068579.
ACCESSION   CQ725283
VERSION   CQ725283.1 GI:42286140
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
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                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE   Nucleic acid arrays, comprising a majority of
                humanexons or transcripts, for detecting expression and other uses
                thereof
  JOURNAL   Patent: WO 02068579-A 11217 06-SEP-2002;
                PE Corporation (NY) (US)
FEATURES   Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
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ORIGIN

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Best Local Similarity   99.6%; Pred. No. 3.9e-220;
Matches 1120; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

[Sequence alignment of Query (Qy) against Database (Db), positions 1–1124, displayed in two columns of paired Qy/Db rows with match bars.]

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                    GenCore version 5.1.7
                    Copyright (c) 1993 - 2006  Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1123	100.0	1123	3	US-09-888-264-1	Sequence 1, Appli
2	968.6	86.3	1503	3	US-09-888-264-2	Sequence 2, Appli
3	968.6	86.3	1570	9	US-10-507-617-12	Sequence 12, Appl
4	945	84.1	945	9	US-10-745-237-369	Sequence 369, Appl
5	802.6	71.5	1091	7	US-10-261-175A-5	Sequence 5, Appli
6	787.2	70.1	946	7	US-10-191-803-147	Sequence 147, App
7	787.2	70.1	946	9	US-10-764-420-492	Sequence 492, App
8	440.2	39.2	552	3	US-09-918-995-10779	Sequence 10779, App
9	362	32.2	418	3	US-09-918-995-953	Sequence 953, App
10	359	32.0	454	3	US-09-918-995-1777	Sequence 1777, App
11	356.6	31.8	1654	10	US-11-097-143-815	Sequence 815, App
12	314.6	28.0	3725	10	US-11-097-143-814	Sequence 814, App
13	308.6	27.5	1205	7	US-10-425-114-26014	Sequence 26014, A
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17	269.4	24.0	14993	8	US-10-741-600-17979	Sequence 17979, A
18	269.4	24.0	17149	8	US-10-741-600-17980	Sequence 17980, A
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23	248.2	22.1	906	10	US-11-097-143-554	Sequence 554, App
c 24	248.2	22.1	2906	10	US-11-097-143-553	Sequence 553, App
c 25	216	19.2	24127	5	US-10-087-192-1039	Sequence 1039, Ap
c 26	201.2	17.9	1650	7	US-10-437-963-23510	Sequence 23510, A
27	180	16.0	1572	8	US-10-425-115-118087	Sequence 118087,
28	169.4	15.1	1898	7	US-10-425-114-6241	Sequence 6241, Ap
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30	157	14.0	1578	7	US-10-424-599-133252	Sequence 133252,
31	153.2	13.6	660	7	US-10-437-963-56406	Sequence 56406, A
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33	143.2	12.8	1414	8	US-10-425-115-30789	Sequence 30789, A
34	143	12.7	1406	7	US-10-425-114-19049	Sequence 19049, A
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c 36	142.4	12.7	366	9	US-10-505-680-545	Sequence 545, App
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41	136.8	12.2	1238	7	US-10-425-114-19387	Sequence 19387, A
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ALIGNMENTS

RESULT 1
US-09-888-264-1
;   Sequence 1, Application US/09888264
;   Patent No. US2002010315041
;   GENERAL INFORMATION:
;   APPLICANT: Adams, Sean
;   APPLICANT: Yu, Xiang Xian
;   TITLE OF INVENTION: CONTROL OF METABOLISM WITH COMPOSITIONS OF THE HUMAN 2-OXOGLUTARA,
;   TITLE OF INVENTION: CARRIER
;   FILE REFERENCE: 10466/35
;   CURRENT APPLICATION NUMBER: US/09/888,264
;   CURRENT FILING DATE: 2001-09-17
;   PRIOR APPLICATION NUMBER: 60/213,307
;   PRIOR FILING DATE: 2000-06-22
;   NUMBER OF SEQ ID NOS: 2
;   SOFTWARE: PatentIn version 3.1
;   SEQ ID NO 1
;   LENGTH: 1123
;   TYPE: DNA
;   ORGANISM: Homo sapiens; GenBank NM_003562
US-09-888-264-1

Query Match   100.0%; Score 1123; DB 3; Length 1123;
Best Local Similarity 100.0%;
Matches 1123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CCGAGGGGCCATTGAGTGGCGGATGGGCGGCGCGACGTGCCGGGCGGCGGGATGGACG   60
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Db          1 CCGAGGGGCCATTGAGTGGCGGATGGGCGGCGCGACGTGCCGGGCGGCGGGATGGACG   60

Qy         61 GGAAGCCCCGTACCTCCCCTAAGTCCGTCAAGTTCCTGTTTGGGGGGCCTGGCCGCGGGATGG  120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAAGCCCCGTACCTCCCCTAAGTCCGTCAAGTTCCTGTTTGGGGGGCCTGGCCGCGGGATGG  120

Qy        121 GAGCTACAGTTTTTGTCCAGCCCCTGGACCCTGGTGAAGAACCCGATGCAGTTGAGCGGCG  180
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Db        121 GAGCTACAGTTTTTGTCCAGCCCCTGGACCCTGGTGAAGAACCCGATGCAGTTGAGCGGCG  180

Qy        181 AAGGGGGCCAAGACTCGAGAGTACAAAACCAGCTTCCATGCCCTCACCAGTATCCTGAAGG  240
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Db        181 AAGGGGGCCAAGACTCGAGAGTACAAAACCAGCTTCCATGCCCTCACCAGTATCCTGAAGG  240

Qy        241 CAGAAGGGCCTGAGGGGCAGTTACACTGGGCGTGTCGGCCTGGCGGCCTGGGCTCAGGCCACCT  300
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RESULT 2
US-09-888-264-2

; Sequence 2, Application US/09888264
; Patent No. US20020315OA1
; GENERAL INFORMATION:
; APPLICANT: Adams, Sean
; APPLICANT: Yu, Xiang Xian
; TITLE OF INVENTION: CONTROL OF METABOLISM WITH COMPOSITIONS OF THE HUMAN 2-OXOGLUTARA
; TITLE OF INVENTION: CARRIER
; FILE REFERENCE: 10466/35
; CURRENT APPLICATION NUMBER: US/09/888,264
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/213,307
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.1

; SEQ ID NO 2
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo sapiens; GenBank AF070548
US-09-888-264-2

Query Match   86.3%; Score 968.6; DB 3; Length 1503;
Best Local Similarity   99.1%; Pred. No. 6.5e-289;
Matches 974; Conservative   0; Mismatches   9; Indels   0; Gaps   0;

Qy   1 CCGAGGGCCATTGAGTGGGCGATGGCGGCGACGGGCGAGTGCGGCCGGCGGGGGATGGACG 60
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Db   92 CCGAGGGCCATTGAGTGGGCGATGGCGGCGACGGGCGAGTGCGGCCGGCGGGGGATGGACG 151

Qy   61 GGAAGCCCCGTACCTCCCCCTCCCCCTAAGTCCGTCAAGTTCCTGTTTTGGGGGGTGGGGG 120
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Db   152 GGAAGCCCCGTACCTCCCCCTCCCCCTAAGTCCGTCAAGTTCCTGTTTTGGGGGGTGGGGG 211

Qy   121 GAGCTACAGTTTTTGTCCAGCCCCCTGGGACTGGTGGAGTGTGAAGAACCGGATGCAGTTG 180
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Qy   181 AAGGGGCCCAAGACTCGAGAGTACAAAAACCAGCTTCCATGCCCTCACCAGTATCCTGAAGG 240
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Qy   241 CAGGAAGGGCTGAGGGGCCATTTACACTGTGGGGCTGGTCGGGCTGGCCTGCGTGCTGCCACCT 300
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Db   332 CAGGAAGGGCCGAGGGGCCATTTACACTGGGGGCTGGTCGGGCTGGCTGCGTGCTGCCACT 391

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Qy   361 GTACTCCCCCTGGCTTTCTGCTGAAGGCTGTGATTGGGCATGACGGGCGACGGCGCAGGTG 420
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Qy   421 CCTTTGTGGGAACACCAGCCCGGAAGTGGCTCTTATCCCGGAATCCAGAACACCACCCGGTG 480
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Db   572 CAGCTGACCCAGCGGCCGTGGCTACAAAAAATGTGTTTAACGGCCCCTGAATTCGAAATCA 631

Qy   541 AAGAGGGGTGTCCTCACACTGTGGGGGGGGGGGGCTGCAGTCAAAGTTGCAGGGGCCTGTCG 600
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Db   632 AAGAGGGGTGTCCTCACACTGTGGGGGGGGGGGGCTGCAGTCAAAGTTGTCAGTGGGGGAAACCA 691

Qy   601 TCAAATGCTGCCCAGCTCGGCCTCCTTACTCCCAATCCAAGCAGTTCTTACTGGACTCAGGCT 660
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Db   692 TCAAATGCTGCCCAGCTCGGCCTCCTTACTCCCAATCCAAGCAGTTCTTACTGGACTCAGGCT 751

Qy   661 ACTTCTCTGACAACATCCTGTGCCACTTCGTGGGGGGGGGCTGGGGCCGGTCGTTGCTCG 720
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Qy   721 CTGCTGCCTCCAGTCCCTGGGGGCAATTGCCAAGACCGGAATCCAGAACATGGCGATGAT 780
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Qy   781 ATGGGGAAGCCGGAATACAAGAACGGGGCTGGACGTGGCTGGTCGTTCAAGTTGTCCGCTACGAGG 840
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Qy   841 GCTTCTTCAGCCGTGTGGAAGGGGCTTCACGGGGTCGGGGCCGCTTCACTGGTG 900
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Qy   901 TCCTTCACCTTCATCTTCTTGGAGGCAGAGGATGAACAAGGCCTACAACGGGTCTCTTCCTCAGTG 960
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Db   992 TCCTTCACCTTCATCTTCTTGGAGGCAGAGGATGAACAAGGCCTACAACGGGTCTCTTCCTCAGTG 1051

Qy   961 GCTGAAGGCGTTTCAGGGGCACAGGACAGCGAGAGTACCCCTTTGTCAGTGGGGGAAACCA 1020
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Qy   1021 AGGCAGAGCTGAGGGAGGGAGGAGGAGGAAGCCATCAAGAGTGGTCAAAGGGCCTGCGTCG 1080
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Qy   1081 AGGGAGAGATGTGGGCCTTCCTCCCCCCCCTCATTGAGAGACTCAATAAA 1123
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: February 1, 2006, 14:41:42 ; Search time 33.9124 Seconds
(without alignments)
2767.263 Million cell updates/sec

Title: US-09-888-264-1
Perfect score: 2181
Sequence: 1 ccgagggccattgagtggcg.................ctcattgaggactcaataaa 1123

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1867569 seqs, 417829326 residues
Listing first 45 summaries

Post-processing: Minimum Match 0%
Maximum Match 100%

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

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-DB=Published_Applications_AA_Main -QFMT=fastan -SUFFIX=rapbm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -HOST=abss02p
-USER=US09888264 @CGN_1_1.405 @runat 01022006 131847 14955 -NCPU=6 -ICPU=3
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Database : Published_Applications_AA_Main:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1604	73.5	314	4	US-10-408-765A-498	Sequence 498, App
2	1600	73.4	314	4	US-10-408-765A-2204	Sequence 2204, Ap
3	1600	73.4	314	4	US-10-408-765A-3015	Sequence 3015, Ap
4	1600	73.4	314	5	US-10-507-617-13	Sequence 13, App
5	1558	73.4	314	5	US-10-745-237-370	Sequence 370, App
6	1517	71.4	314	5	US-10-507-617-57	Sequence 57, Appl
7	1056	69.6	297	5	US-10-507-617-56	Sequence 56, Appl
8	1056	48.4	310	4	US-10-425-115-211662	Sequence 211662,
9	1056	48.4	312	4	US-10-425-115-59754	Sequence 59754, A
10	1052	48.2	323	4	US-10-365-493-5321	Sequence 5321, Ap
11	926.5	42.5	344	5	US-10-732-923-19208	Sequence 19208, A

12	915.5	42.0	317	5	US-10-732-923-19321	Sequence 19321, A
13	915.5	42.0	317	5	US-11-097-143-816	Sequence 816, Appl
14	839.5	38.5	294	5	US-10-507-617-55	Sequence 55, Appl
15	839.5	38.5	311	5	US-10-732-923-19320	Sequence 19320, A
16	839.5	38.5	311	6	US-10-507-617-58	Sequence 58, Appl
17	839.5	38.5	311	6	US-11-097-143-27690	Sequence 27690, A
18	838.5	38.4	311	6	US-10-732-923-19319	Sequence 19319, A
19	782	35.9	301	6	US-10-732-923-19326	Sequence 19326, A
20	782	35.9	301	5	US-11-097-143-168	Sequence 168, App
21	782	35.9	301	5	US-10-745-237-168	Sequence 555, App
22	610	28.0	308	4	US-10-437-963-154439	Sequence 154439,
23	607	27.8	308	4	US-10-767-701-45989	Sequence 45989, A
24	602.5	27.6	302	4	US-10-425-114-47724	Sequence 47724, A
25	599	27.5	344	4	US-10-732-923-19256	Sequence 19256, A
26	599	27.5	301	4	US-10-424-599-220995	Sequence 220995,
27	598	27.4	302	4	US-10-732-923-19255	Sequence 19255, A
28	597.5	27.4	349	4	US-10-425-114-47829	Sequence 47829, A
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32	592	27.1	311	4	US-10-425-115-264201	Sequence 264201,
33	590	27.1	300	5	US-10-732-923-19241	Sequence 19241, A
34	589	27.0	317	4	US-10-424-599-276095	Sequence 276095,
35	589	27.0	341	4	US-10-425-114-52234	Sequence 52234, A
36	587	26.9	297	5	US-10-732-923-19942	Sequence 19942, A
37	586	26.9	285	4	US-10-424-599-276094	Sequence 276094,
38	585.5	26.8	285	4	US-10-425-114-41594	Sequence 41594, A
39	585	26.8	295	5	US-10-732-923-19244	Sequence 19244, A
40	585	26.8	327	4	US-10-437-963-125993	Sequence 125993,
41	585	26.8	315	4	US-10-425-115-264201	Sequence 264201,
42	583	26.7	297	5	US-10-732-923-19247	Sequence 19247, A
43	580.5	26.6	300	4	US-10-424-599-217619	Sequence 217619,
44	535.5	24.6	1796	5	US-10-732-923-19283	Sequence 19283, A
45	529	24.3	290	4	US-10-425-115-302750	Sequence 302750,

RESULT 1
US-10-408-765A-498

; Sequence 498, Application US/10408765A

; Publication No. US20040101874A1

GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 498
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-498

Alignment Scores:
Score: 1604.00
Pred. No.: 5.32e-120
Percent Similarity: 100.0%
Percent Identity: 100.0%
Best Local Similarity: 73.5%
Query Match: 4

Length:	314	Matches:	314
Conservative:	0	Mismatches:	0
Indels:	0	Gaps:	0

DB:

US-09-888-264-1 (1-1123) x US-10-408-765A-498 (1-314)

ALIGNMENTS

; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2204
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2204

Alignment Scores:
Pred. No.:
Score: 1600.00
Percent Similarity: 100.0%
Best Local Similarity: 99.7%
Query Match: 4

Length: 314   1.11e-119
Matches: 313
Conservative: 1
Mismatches: 0
Indels: 0
Gaps: 0

US-09-888-264-1 (1-1123) x US-10-408-765A-2204 (1-314)

Qy   21 ATGGCGGCGGACGCGGGAGTGCCGGGGGGCCGGGGGGATGAGGACGGGAGCCCGTACTTCCCT 80
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         MetAlaAlaThrAlaSerAlaGlyAlaGlyValLysProArgThrSerPro 20

Qy   81 AAGTCCGTCAAGTTCCTGTTTGGGGGGCCTGGCCCGGGGATGGGAGCTACAGTTTTTGTCCAG 140
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Qy 261 TACACTGGGCGTGCTGGGCTGCCCACCTACACCACTACCCCGCCTTGGC 320
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Qy 321 ATCTATACCGGTGCTGTTTGAGCCCGACTGGGCGGCGAGTCCCCCTGGCTTTCTG 380
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Db 121 LeuLysAlaValIleGlyMetThrAlaGlyAlaThrGlyAlaPheValGlyThrProAla 140

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Qy 681 TGCCACTTCTGTGCCAGCATGATCAGCGGCGTCTTGTCACCACTGCTGCCTTCCAATGCCTGTG 740
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Qy 861 GGCTTCACGCCGTACTATGCCCGGGCGCCCCACACCGTCTCACCTTCACTTCTTG 920
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Db 301 GluGlnMetAsnLysAlaTyrLysArgValSerProSerVal 314

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: February 1, 2006, 13:54:36 ; Search time 7.48382 Seconds
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Title: US-09-888-264-1
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Issued_Patents_AA:*
                 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
                 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
                 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
                 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	% DB	DB ID	Description
1	586	26.9	299	2	US-09-463-239-35	Sequence 35, Appl
2	513	23.5	313	2	US-09-248-796A-17621	Sequence 17621, A
3	507.5	23.3	355	2	US-09-463-239-30	Sequence 30, Appl
4	500	22.9	322	2	US-09-949-016-8722	Sequence 8722, Ap
5	500	22.9	322	2	US-09-949-016-8723	Sequence 8723, Ap
6	500	22.9	335	2	US-09-482-273-118	Sequence 118, App
7	495	22.7	290	2	US-09-743-847-2	Sequence 2, Appli
8	468.5	21.5	300	2	US-09-463-239-34	Sequence 34, Appl
9	444	20.4	432	1	US-09-463-239-3	Sequence 3, Appli
10	444	20.4	432	1	US-08-937-466-4	Sequence 4, Appl
11	444	20.4	432	1	US-09-172-528-1	Sequence 4, Appli
12	444	20.4	432	2	US-09-503-579-4	Sequence 4, Appli
13	440	20.2	308	1	US-08-937-466-2	Sequence 2, Appli
14	440	20.2	308	1	US-09-172-528-2	Sequence 2, Appli
15	440	20.2	308	2	US-09-318-199-2	Sequence 2, Appli
16	440	20.2	308	2	US-09-503-579-2	Sequence 2, Appli
17	438.5	20.1	307	2	US-09-743-847-3	Sequence 3, Appli
18	438.5	20.1	307	2	US-10-037-417-87	Sequence 87, Appl
19	438.5	20.1	309	2	US-09-949-016-10401	Sequence 10401, A
20	435.5	20.0	306	2	US-10-009-962-5	Sequence 5, Appli
21	435.5	20.0	306	2	US-09-671-628-5	Sequence 5, Appli
22	433.5	19.9	291	2	US-09-501-558-2	Sequence 2, Appli
23	430.5	19.7	307	2	US-10-037-417-88	Sequence 88, Appl
24	430.5	19.7	307	2	US-09-671-628-7	Sequence 7, Appli
25	428.5	19.6	312	2	US-09-808-457-2	Sequence 2, Appli
26	426	19.5	312	2	US-10-009-962-7	Sequence 7, Appli
27	426	19.5	312	2	US-09-142-565-2	Sequence 2, Appli
28	426	19.5	312	2	US-09-808-457-2	Sequence 2, Appli
29	426	19.5	312	2	US-09-671-628-9	Sequence 9, Appli
30	424	19.4	310	2	US-10-009-962-9	Sequence 9, Appli
31	418	19.2	310	2	US-09-743-847-5	Sequence 5, Appli
32	415.5	19.1	307	1	US-08-807-861A-56	Sequence 56, Appli
33	415.5	19.1	307	2	US-09-210-681-56	Sequence 56, Appli
34	415.5	19.1	307	2	US-09-946-719A-56	Sequence 56, Appli
35	415.5	19.1	307	2	US-09-547-983-56	Sequence 56, Appli
36	415.5	19.1	307	2	US-10-037-417-91	Sequence 91, Appl
37	412	18.9	337	2	US-09-949-016-9410	Sequence 9410, Ap
38	411.5	18.9	309	2	US-09-743-847-4	Sequence 4, Appli
39	411.5	18.9	309	2	US-10-041-051B-2	Sequence 2, Appli
40	411.5	18.9	309	2	US-09-671-628-8	Sequence 8, Appli
41	410.5	18.8	299	2	US-08-518-878B-56	Sequence 56, Appli
42	410.5	18.8	299	2	US-08-470-868A-56	Sequence 56, Appli
43	410.5	18.8	309	1	US-08-518-878B-51	Sequence 51, Appl
44	410.5	18.8	309	1	US-08-807-861A-51	Sequence 51, Appl
45	410.5	18.8	309	1	US-08-470-868A-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1
US-09-463-239-35

Sequence 35, Application US/0946323239

Patent No. 6700039

GENERAL INFORMATION:

;   APPLICANT: Jepson, Ian
;   APPLICANT: Ebneth, Marcus
;   APPLICANT: Sonnewald, Uwe
;   TITLE OF INVENTION: Genetic Method for Controlling Sprouting
;   FILE REFERENCE: 109846.178
;   CURRENT APPLICATION NUMBER: US/09/463,239
;   CURRENT FILING DATE: 2000-01-21
;   PRIOR APPLICATION NUMBER: PCT/GB98/02023
;   PRIOR FILING DATE: 1998-07-10
;   PRIOR APPLICATION NUMBER: EP 97113118.0
;   PRIOR FILING DATE: 1997-07-30
;   NUMBER OF SEQ ID NOS: 39
;   SOFTWARE: PatentIn version 3.0
;   SEQ ID NO 35
;   LENGTH: 299
;   TYPE: PRT
;   ORGANISM: Panicum millaceum
;

US-09-888-264-1
US-09-463-239-35

Alignment Scores:
Pred. No.:   7.12e-46
Score: 586.00   Length: 299
Percent Similarity: 61.2%   Matches: 137
Best Local Similarity: 47.4%   Conservative: 40
Query Match: 26.9%   Mismatches: 94
DB: 2   Indels: 18
                                        Gaps: 7

Qy   US-09-888-264-1 (1-1123) x US-09-463-239-35 (1-299)

Qy   93 TTCCTGTTTGGGGGGCCTGGCCCGGATGGGAGCTACACAGTTTTTGTGTCCAGCCCCTGGACCTG 152
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RESULT 2
US-09-248-796A-17621
Sequence 17621, Application US/0924879GA
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 17621
LENGTH: 313
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-17621

Alignment Scores:
Pred. No.:
Score: 4.44e-39
                            513.00
Percent Similarity: 57.3%
Best Local Similarity: 37.6%
Query Match: 23.5%
DB: 2

Length: 313
Matches: 111
Conservative: 58
Mismatches: 108
Indels: 18
Gaps: 4

US-09-888-264-1 (1-1123) x US-09-248-796A-17621 (1-313)